

10/770117

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DICTIONARY FILE UPDATES: 23 JAN 2006 HIGHEST RN 872490-64-7

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*

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<http://www.cas.org/ONLINE/UG/regprops.html>

L1 4 S DLMGYIPAV/SQSP

L1 ANSWER 1 OF 4 REGISTRY COPYRIGHT 2006 ACS on STN
RN 827608-26-4 REGISTRY
CN L-Leucine, L- α -aspartyl-L-leucyl-L-methionylglycyl-L-tyrosyl-L-
isoleucyl-L-prolyl-L-alanyl-L-valylglycyl-L-alanyl-L-prolyl- (9CI)
(CA INDEX NAME)

OTHER NAMES:

CN 4: PN: WO2005004910 PAGE: 51 claimed sequence
SQL 13

SEQ 1 DLMGYIPAVG APL
=====

HITS AT: 1-9

REFERENCE 1: 142:154229

L1 ANSWER 2 OF 4 REGISTRY COPYRIGHT 2006 ACS on STN
RN 260232-79-9 REGISTRY
CN Hepatitis C core antigen [139-alanine] (hepatitis C virus) (9CI) (CA
INDEX NAME)
OTHER NAMES:

Searcher : Shears 571-272-2528

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10/770117

CN 1: PN: WO0011186 SEQID: 2 claimed protein
CI MAN
SQL 191

SEQ 1 MSTNPKPQKK NKRNTNRRPQ DVKFPGGGQI VGGVYLLPRR GPRLGVRATR
51 KTSERSQPRG RRQPIPKARR PEGRTWAQPG YPWPLYGNEG CGWAGWLLSP
101 RGSRPSWGPT DPRRRSRNLG KVIDTLTCGF ADLMGYIPAV GAPLGGAARA
=====

151 LAHGVRVLED GVNYATGNLP GCSFSIFLLA LLSCLTVPAS A

HITS AT: 132-140

REFERENCE 1: 132:206926

L1 ANSWER 3 OF 4 REGISTRY COPYRIGHT 2006 ACS on STN
RN 215295-45-7 REGISTRY
CN L-Valine, L- α -aspartyl-L-leucyl-L-methionylglycyl-L-tyrosyl-L-
isoleucyl-L-prolyl-L-alanyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 12: PN: WO2004084938 PAGE: 27 claimed sequence
CN 1: PN: WO0011186 SEQID: 1 claimed protein
CN 48: PN: WO2005004910 PAGE: 52 claimed sequence
SQL 9

SEQ 1 DLMGYIPAV
=====

HITS AT: 1-9

REFERENCE 1: 143:373377

REFERENCE 2: 142:154229

REFERENCE 3: 141:409214

REFERENCE 4: 141:330768

REFERENCE 5: 134:285564

REFERENCE 6: 132:206926

REFERENCE 7: 129:329617

L1 ANSWER 4 OF 4 REGISTRY COPYRIGHT 2006 ACS on STN
RN 199533-14-7 REGISTRY
CN L-Valine, L-alanyl-L- α -aspartyl-L-leucyl-L-methionylglycyl-L-
tyrosyl-L-isoleucyl-L-prolyl-L-alanyl- (9CI) (CA INDEX NAME)
SQL 10

SEQ 1 ADLMGYIPAV
=====

HITS AT: 2-10

REFERENCE 1: 128:33617

FILE 'CAPLUS' ENTERED AT 16:48:58 ON 24 JAN 2006
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FILE COVERS 1907 - 24 Jan 2006 VOL 144 ISS 5
FILE LAST UPDATED: 23 Jan 2006 (20060123/ED)

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<http://www.cas.org/infopolicy.html>

L2 8 L1

L2 ANSWER 1 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN

ED Entered STN: 14 Oct 2005

ACCESSION NUMBER: 2005:1103622 CAPLUS

DOCUMENT NUMBER: 143:373377

TITLE: Method for solubilizing peptide mixtures

INVENTOR(S): Zauner, Wolfgang; Kritsch, Constantia;
Heinrich-Cseh, Christa; Berger, Agnes

PATENT ASSIGNEE(S): Intercell AG, Austria

SOURCE: PCT Int. Appl., 21 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2005094891	A2	20051013	WO 2005-EP2583	20050311
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW			
RW:	BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			

PRIORITY APPLN. INFO.: EP 2004-450061 A 20040312

AB Described is a method for making a pharmaceutical preparation comprising the solubilization of a peptide mixture, characterized in that the peptide mixture is solubilized by an aqueous solution containing at least one organic acid selected from the group consisting of formic acid, acetic acid, propionic acid, butyric acid and halogenated or hydroxylated forms thereof.

IT 215295-45-7

RL: PEP (Physical, engineering or chemical process); PRP (Properties); PYP (Physical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(method for solubilizing peptide mixts.)

L2 ANSWER 2 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN

ED Entered STN: 20 Jan 2005

ACCESSION NUMBER: 2005:55094 CAPLUS

DOCUMENT NUMBER: 142:154229

TITLE: Hepatitis C virus vaccines comprise HLA-A2, -DR1 and -DR7 epitopes and immune adjuvant

INVENTOR(S): Buschle, Michael; Frisch, Juergen; Klade, Christoph; Lingnau, Karen; Zauner, Wolfgang; Zettlmeissl, Gerd

PATENT ASSIGNEE(S): Intercell AG, Austria

SOURCE: PCT Int. Appl., 59 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 7

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2005004910	A2	20050120	WO 2004-EP7540	20040709
WO 2005004910	A3	20050421		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW			
RW:	BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			

PRIORITY APPLN. INFO.: EP 2003-450171 A 20030711

EP 2004-450062 A 20040312

OTHER SOURCE(S): MARPAT 142:154229

AB Disclosed is a Hepatitis C virus (HCV) vaccine comprising at least two epitopes, each from a different hotspot epitope, wherein a hotspot epitope is defined as an epitope containing peptide selected from the group consisting of KFPGGGQIVGGVYLLPRRGPRLGVRATRK, GYKVLVLNPSVAAT, AYAAQGYKVLVLNPSVAAT, DLMGYIP(A/L)VGAPL, GEVQVVSTATQSFLATCINGVCWTV, HMWNFISGIQYLAGLSTLPGNPA, VDYPYRLWHYPCT(V/I)N(F/Y)TIFK(V/I)RMYVGGVEHRL, AAWYELTPAETTVRLR, GQGWRLAPITAYSQQTRGLLGCIIV, IGLGKVLVDILAGYGAGVAGALVAFK, FTDNSSPPAVPQTFQV, LEDRDRSELSPLLLSTTEW, YLVAYQATVCARAQAPPPSWD, MSTNPKPQRKTKRNTNR, LINTNGSWHINRTALNCNDSL, TTILGIGTVLDQAET, FDS(S/V)VLCECYDAG(A/C)AWYE, ARLIVFPDLGVRVCEKMALY, AFCSAMYVGDLGSGV, GVLFGLAYFSMVGNW, VVCCSMSYTTWTGALITPC, TRVPYFVRAQGLIRA and TTLLFNILGGWVAAQ.

IT 215295-45-7 827608-26-4

RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

10/770117

(HCV vaccines comprise HLA-A2, -DR1 and -DR7 epitopes and immune adjuvant)

L2 ANSWER 3 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN
 ED Entered STN: 07 Oct 2004
 ACCESSION NUMBER: 2004:817738 CAPLUS
 DOCUMENT NUMBER: 141:330768
 TITLE: Vaccines comprising antigen, polycationic peptide and immunostimulatory deoxynucleic acid against viral infection
 INVENTOR(S): Buschle, Michael; Habel, Andre; Fritz, Joerg; Prinz, Karin; Lingnau, Karen
 PATENT ASSIGNEE(S): Intercell A.-G., Austria
 SOURCE: PCT Int. Appl., 62 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 7
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004084938	A1	20041007	WO 2004-EP3002	20040322
W:			AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW	
RW:			BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG	
CA 2517673	AA	20041007	CA 2004-2517673	20040322
EP 1608402	A1	20051228	EP 2004-722281	20040322
R:			AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, PL, SK	
PRIORITY APPLN. INFO.:			EP 2003-450072	A 20030324
			EP 2003-450084	A 20030411
			EP 2003-450171	A 20030711
			WO 2004-EP3002	W 20040322

AB The invention refers to an improved vaccine against infections with pathogens, especially viral pathogens, comprising an antigen, a peptide of the formula R1-XZXZN-XZX-R2 and an immunostimulatory deoxynucleic acid containing deoxyinosine and/or deoxyuridine residues. Prepared were influenza vaccine compns. and hepatitis B vaccine compns.

IT 215295-45-7

RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (vaccines comprising antigen, polycationic peptide and immunostimulatory deoxynucleic acid against viral infection)

REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR

Searcher : Shears 571-272-2528

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THIS RECORD. ALL CITATIONS AVAILABLE IN THE
RE FORMAT

L2 ANSWER 4 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN
ED Entered STN: 19 Apr 2004
ACCESSION NUMBER: 2004:313986 CAPLUS
DOCUMENT NUMBER: 141:409214
TITLE: Detection of serum heat shock protein 70 level in
patients with hepatitis C infection and its role
in cytotoxicity of CTLs induced by HSP70-HCV
peptide complex
AUTHOR(S): Men, Ke; Wang, Xia; Xu, Dezhong; Zhou, Hongchao;
Zhang, Jingxia
CORPORATE SOURCE: Division of Preventive Medicine, Fourth Military
Medical University, Xian, Shanxi Province, 710032,
Peop. Rep. China
SOURCE: Xibao Yu Fenzi Mianyxue Zazhi (2003), 19(3),
305-307
CODEN: XFMZFM; ISSN: 1007-8738
PUBLISHER: Xibao Yu Fenzi Mianyxue Zazhi Bianjibu
DOCUMENT TYPE: Journal
LANGUAGE: Chinese
AB The serum HSP70 in patients with hepatitis C was detected and its role
in cytotoxicity of specific CTLs induced by HSP70-HCV peptide complex
was evaluated. The serum HSP70 level in patients infected with HCV
and normal individuals were detected by ELISA. The relationship
between anti-HCV antibody and HSP70 was evaluated. Peripheral blood
mononuclear cells (PBMCs) were activated by HSP70-HCV peptide complex
and then 4 h ⁵¹Cr release assay were used to detect the killer
activity of CTLs. Detection rates of HSP70 were 82.1% (22/28) and
18.8% (9/48) in patients with anti-HCV antibody and in normal
individuals, resp. There was significant correlation between the
detection rate of HSP70 and HCV infection ($\chi^2=28.77$, $P<0.01$). The
level of serum HSP70 in patients infected with HCV was markedly more
higher than that in normal individuals. CTLs from one patient induced
by HSP70-HCV C region peptide (DLMGYIPAV) complex could lyse
autologous B lymphoblastoid cell lines (BLCLs) with killer rate of
37.8%, whereas CTLs induced by peptide alone could not lyse autologous
BLCLs cells. HCV infection can induce over expression of HSP70.
HSP70 may have the action of enhancing presentation of HCV epitope
peptide and promoting clearance cells infected with HCV.
IT 215295-45-7
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(HSP70-HCV C region peptide complex cytotoxicity in patients with
hepatitis C infection)

L2 ANSWER 5 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN
ED Entered STN: 13 Apr 2001
ACCESSION NUMBER: 2001:265271 CAPLUS
DOCUMENT NUMBER: 134:285564
TITLE: Pharmaceutical composition comprising an antigen
INVENTOR(S): Fleitmann, Julia-Kristina; Mattner, Frank;
Buschle, Michael; Melling, Jack
PATENT ASSIGNEE(S): Cistem Biotechnologies G.m.b.H., Austria
SOURCE: PCT Int. Appl., 20 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1

Searcher : Shears 571-272-2528

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001024822	A2	20010412	WO 2000-EP9657	20001002
WO 2001024822	A3	20011220		
W: AU, BR, CA, CN, CZ, HU, ID, IN, IS, JP, KR, MX, NO, NZ, PL, SG, SK, US, ZA, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AT 9901680	A	20010715	AT 1999-1680	19991001
AT 408721	B	20020225		
EP 1218031	A2	20020703	EP 2000-969387	20001002
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY				
US 2003099663	A1	20030529	US 2002-114823	20020401
US 2005163797	A1	20050728	US 2005-82595	20050317
PRIORITY APPLN. INFO.:			AT 1999-1680	A 19991001
			WO 2000-EP9657	W 20001002
			US 2002-114823	A1 20020401

AB The inventions discloses a pharmaceutical composition comprising an antigen, an immunostimulating substance selected from neuroactive compds., hormones, compds. having a growth hormone activity, and mixts. thereof, and a polycationic polymer.

IT 215295-45-7

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PEP (Physical, engineering or chemical process); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(pharmaceutical composition comprising an antigen)

L2 ANSWER 6 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN

ED Entered STN: 03 Mar 2000

ACCESSION NUMBER: 2000:145039 CAPLUS

DOCUMENT NUMBER: 132:206926

TITLE: Modified HCV peptide vaccines

INVENTOR(S): Berzofsky, Jay A.; Sarobe, Pablo; Pendleton, C. David; Feinstone, Stephen M.; Arichi, Tatsumi; Major, Marian E.

PATENT ASSIGNEE(S): United States Dept. of Health and Human Services, USA

SOURCE: PCT Int. Appl., 78 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000011186	A1	20000302	WO 1999-US18674	19990817
WO 2000011186	C2	20020822		
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE,				

10/770117

SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA,
ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE,
DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ,
CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
AU 9957767 A1 20000314 AU 1999-57767 19990817
EP 1105496 A1 20010613 EP 1999-945074 19990817
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,
PT, IE, SI, LT, LV, FI, RO
US 6685944 B1 20040203 US 2001-763260 20011019
US 2005129705 A1 20050616 US 2004-770117 20040202
PRIORITY APPLN. INFO.: US 1998-97446P P 19980821
WO 1999-US18674 W 19990817
US 2001-763260 A3 20011019

AB The present invention provides (1) an isolated peptide having the amino acid sequence DLMGYIPAV, (SEQ ID NO: 1); (2) an isolated HCV core polypeptide comprising an L→A substitution at amino acid position 139; (3) an isolated HCV core polypeptide having the amino acid sequence of SEQ ID NO: 2; and (4) a fragment of an HCV core polypeptide having fewer amino acids than the entire HCV core polypeptide and comprising the amino acid sequence SEQ ID NO: 1. Also provided are nucleic acids which encode the peptides and polypeptides of this invention, vectors comprising the nucleic acids of this invention and cells comprising the vectors and nucleic acids of this invention. The present invention further provides methods of producing an immune response in a subject and/or treating or preventing HCV infection in a subject, comprising administering to the subject, or to a cell of the subject, any of the compns. of this invention. The present invention also provides methods for determining a viral load and prognosis of a subject diagnosed with hepatitis C virus infection.

IT 260232-79-9

RL: PRP (Properties)

(amino acid sequence; modified HCV peptides as vaccines and for determination of virus load or prognosis of HCV infection)

IT 215295-45-7

RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(modified HCV peptides as vaccines and for determination of virus load or prognosis of HCV infection)

REFERENCE COUNT:

6

THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 7 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN

ED Entered STN: 30 Sep 1998

ACCESSION NUMBER: 1998:618237 CAPLUS

DOCUMENT NUMBER: 129:329617

TITLE:

Enhanced in vitro potency and in vivo immunogenicity of a CTL epitope from hepatitis C virus core protein following amino acid replacement at secondary HLA-A2.1 binding positions

AUTHOR(S):

Sarobe, Pablo; Pendleton, C. David; Akatsuka, Toshitaka; Lau, Daryl; Engelhard, Victor H.; Feinstone, Stephen M.; Berzofsky, Jay A.

Searcher : Shears 571-272-2528

CORPORATE SOURCE: Molecular Immunogenetics and Vaccine Research
Section, Metabolism Branch, National Cancer
Institute, National Institutes of Health,
Bethesda, MD, 20892, USA

SOURCE: Journal of Clinical Investigation (1998), 102(6),
1239-1248
CODEN: JCINAO; ISSN: 0021-9738

PUBLISHER: Rockefeller University Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Since the natural immune response to hepatitis C virus (HCV) is often
unable to clear the infection, to enhance immunogenicity we studied
substituted peptides from an HCV cytotoxic T lymphocyte (CTL) epitope
(C7A2) from a conserved region of the HCV core protein (DLMGYIPLV)
recognized by CTL lines from HLA-A2.1+ HCV-infected patients and
HLA-A2.1 transgenic mice. HLA-A2.1 binding, human and murine CTL
recognition, and in vivo immunogenicity (using mice transgenic for
human HLA-A2 in lieu of immunizing humans) were analyzed to define
peptides with enhanced immunogenicity. Peptides substituted at
position 1 showed enhanced HLA-A2 binding affinity, but paradoxically
poorer immunogenicity. A peptide with Ala substituted at position 8
(8A) showed higher HLA-A2 binding affinity and CTL recognition and was
a more potent in vivo immunogen in HLA-A2-transgenic mice, inducing
higher CTL responses with higher avidity against native C7A2 than
induced by C7A2 itself. These results suggest that peptide 8A is a
more potent in vitro antigen and in vivo immunogen than C7A2 and may
be useful as a vaccine component. They provide proof of principle
that the strategy of epitope enhancement can enhance immunogenicity of
a CTL epitope recognized by human CTL.

IT 215295-45-7P
RL: BAC (Biological activity or effector, except adverse); BPR
(Biological process); BSU (Biological study, unclassified); SPN
(Synthetic preparation); BIOL (Biological study); PREP (Preparation);
PROC (Process)
(enhanced potency and immunogenicity of CTL epitope from hepatitis
C virus core protein following amino acid replacement at secondary
HLA-A2.1 binding positions)

REFERENCE COUNT: 69 THERE ARE 69 CITED REFERENCES AVAILABLE FOR
THIS RECORD. ALL CITATIONS AVAILABLE IN THE
RE FORMAT

L2 ANSWER 8 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN

ED Entered STN: 17 Nov 1997

ACCESSION NUMBER: 1997:725337 CAPLUS

DOCUMENT NUMBER: 128:33617

TITLE: Immunological significance of cytotoxic T
lymphocyte epitope variants in patients
chronically infected by the hepatitis C virus

AUTHOR(S): Chang, Kyong-Mi; Rehmann, Barbara; Mchutchison,
John G.; Pasquinelli, Claudio; Southwood, Scott;
Sette, Alessandro; Chisari, Francis V.

CORPORATE SOURCE: Department of Molecular & Experimental Medicine,
The Scripps Research Institute, La Jolla, CA, CA
92037, USA

SOURCE: Journal of Clinical Investigation (1997), 100(9),
2376-2385
CODEN: JCINAO; ISSN: 0021-9738

PUBLISHER: Rockefeller University Press

DOCUMENT TYPE: Journal

10/770117

LANGUAGE: English

AB This study was performed to test the hypothesis that cytotoxic T lymphocyte (CTL) selection of hepatitis C virus (HCV) escape variants plays a role in HCV persistence. The peripheral blood CTL responsiveness of patients with well-established chronic hepatitis C to a panel of 10 prototype HCV peptides (genotype 1a) was compared with the corresponding sequences encoded by the infecting viruses in each patient. Variant viral peptide sequences were threefold more frequent in the presence of a CTL response than in its absence, and CTL responses were detected nearly twice as often in association with variant rather than with prototype viral peptide sequences. Furthermore, over half of the patients were infected with potential CTL escape variants that contained nonimmunogenic and noncross-reactive variant peptides many of which displayed reduced HLA-binding affinity. Surprisingly, follow up anal. over a period of up to 46 mo revealed that, in contrast to the relatively high frequency of escape variants initially observed, the subsequent emergence rate of CTL escape variants was very low. Interestingly, the one escape variant that was detected proved to be a CTL antagonist. Collectively, these observations suggest that CTL selection of epitope variants may have occurred in these patients before their entrance into the study and that it may have played a role in HCV persistence. The low apparent rate of ongoing CTL selection in chronically infected patients, however, suggests that if CTL escape occurs during HCV infection it is probably an early event.

IT 199533-14-7P

RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation); PROC (Process)
(cytotoxic T lymphocytes of humans with chronic hepatitis C virus infection reactivity with viral variant epitope)

REFERENCE COUNT: 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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L3 0 L1

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4 SEA ABB=ON PLU=ON DLMGYIPAV/SQSP

FILE 'REGISTRY' ENTERED AT 16:48:57 ON 24 JAN 2006
D 1-4 .BEVREG1

L2 FILE 'CAPLUS' ENTERED AT 16:48:58 ON 24 JAN 2006
8 SEA ABB=ON PLU=ON L1
D 1-8 .BEVSTR

L3 FILE 'MEDLINE, BIOSIS, EMBASE' ENTERED AT 16:49:08 ON 24 JAN 2006
0 SEA ABB=ON PLU=ON L1

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FILE MEDLINE

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On December 11, 2005, the 2006 MeSH terms were loaded.

The MEDLINE reload for 2006 will soon be available. For details on the 2005 reload, enter HELP RLOAD at an arrow prompt (=>). See also:

<http://www.nlm.nih.gov/mesh/>
http://www.nlm.nih.gov/pubs/techbull/nd04/nd04_mesh.html
http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_med_data_changes.ht
http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_2006_MeSH.html

OLDMEDLINE is covered back to 1950.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2006 vocabulary.

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FILE BIOSIS

FILE COVERS 1969 TO DATE.

CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 19 January 2006 (20060119/ED)

FILE EMBASE

FILE COVERS 1974 TO 19 Jan 2006 (20060119/ED)

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FILE HOME

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OM protein - protein search, using sw model

Run on: January 20, 2006, 22:23:12 ; Search time 77 Seconds
(without alignments)
51.356 Million cell updates/sec

Title: US-10-770-117-1
Perfect score: 47
Sequence: 1 DLNGYIPAV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	9	3	AAY82996
2	47	100.0	9	4	AAB82052
3	47	100.0	9	8	ADS97427
4	47	100.0	9	9	ADV96878
5	47	100.0	9	9	ADV96796
6	47	100.0	9	9	ADV96890
7	47	100.0	9	9	ADV96886
8	47	100.0	9	9	ADV96961
9	47	100.0	9	9	ADV96912
10	47	100.0	9	9	ADV96917
11	47	100.0	191	3	AAY82997
12	43	91.5	9	8	ADV98674
13	43	91.5	13	9	ADV96979
14	43	91.5	15	8	ADL25899
15	43	91.5	15	8	ADL25901
16	43	91.5	15	8	ADL25905
17	43	91.5	15	8	ADL25909
18	43	91.5	15	8	ADL25901
19	43	91.5	15	8	ADL25903
20	43	91.5	15	8	ADL25902
21	43	91.5	36	8	ADL26466
22	43	91.5	168	2	AAR52735
23	43	91.5	168	2	AAR49831
24	43	91.5	188	2	AAW41753

25	43	91.5	190	5	AAB71257
26	43	91.5	191	2	AAR92960
27	43	91.5	191	2	AAR92961
28	43	91.5	191	2	AAR92978
29	43	91.5	191	2	AAR92966
30	43	91.5	191	2	AAR92987
31	43	91.5	191	2	AAR92959
32	43	91.5	191	2	AAR92963
33	43	91.5	191	2	AAR92964
34	43	91.5	191	2	AAR92965
35	43	91.5	191	2	AAR92967
36	43	91.5	191	2	AAR92962
37	43	91.5	193	2	AAW41755
38	43	91.5	209	6	ABP55560
39	43	91.5	209	6	ABP55559
40	43	91.5	209	6	ABP55564
41	43	91.5	209	6	ABP55565
42	43	91.5	209	6	ABP55566
43	43	91.5	209	6	AAE32872
44	43	91.5	209	6	AAE32877
45	43	91.5	209	6	AAE32878
46	43	91.5	209	6	AAE32873
47	43	91.5	312	8	ADL17784
48	43	91.5	318	2	AAR96563
49	43	91.5	319	2	AAR63349
50	43	91.5	319	2	AAR96547
51	43	91.5	319	2	AAR96534
52	43	91.5	328	2	AAR67628
53	43	91.5	378	2	AAR50076
54	43	91.5	378	8	ADJ81681
55	43	91.5	515	2	AAR4088
56	43	91.5	515	2	AAR38280
57	43	91.5	719	2	AAR38282
58	43	91.5	737	2	AAR38281
59	43	91.5	1217	2	AAR49832
60	43	91.5	2940	7	ADC42917
61	43	91.5	3010	9	ADX40795
62	43	91.5	3010	9	ADX40792
63	43	91.5	3013	9	ADX40826
64	43	91.5	3015	4	AAB30733
65	43	91.5	3015	4	AAB30731
66	43	91.5	3015	4	AAB30730
67	43	91.5	3015	4	AAB30732
68	43	91.5	3016	9	ADX40827
69	43	91.5	3019	9	ADX40822
70	43	91.5	3033	2	AAR33214
71	43	91.5	3033	2	AAR33538
72	43	91.5	3033	2	AAR33539
73	43	91.5	3033	4	AAE59172
74	43	91.5	3033	4	AAE31168
75	43	91.5	3033	4	AAB30729
76	43	91.5	3033	5	ABG30688
77	43	91.5	3033	9	ADV04738
78	43	91.5	3033	9	ADX40787
79	43	91.5	3033	9	ADX40815
80	43	91.5	3033	9	ADX40819
81	43	91.5	3037	9	ADX40778
82	42	89.4	9	2	AAR73111
83	42	89.4	9	2	AAR59125
84	42	89.4	9	2	AAR78946
85	42	89.4	9	2	AAR78946
86	42	89.4	9	2	AAR78946
87	42	89.4	9	2	AAW39446
88	42	89.4	9	2	AAW54635
89	42	89.4	9	2	AAV10219
90	42	89.4	9	2	AAV10219
91	42	89.4	9	2	AAV10441
92	42	89.4	9	3	AAV73106
93	42	89.4	9	4	AAJ03866
94	42	89.4	9	4	AAJ01746
95	42	89.4	9	4	AAJ03864
96	42	89.4	9	4	AAJ00011
97	42	89.4	9	4	AAJ00229

Aab71257	HCV type
Aar92960	Hepatitis
Aar92961	Hepatitis
Aar92978	Hepatitis
Aar92966	Hepatitis
Aar92987	Hepatitis
Aar92959	Hepatitis
Aar92963	Hepatitis
Aar92964	Hepatitis
Aar92965	Hepatitis
Aar92967	Hepatitis
Aar92962	Hepatitis
AAW41755	Hepatitis
ABP55560	Hepatitis
ABP55559	Hepatitis
ABP55564	Hepatitis
ABP55565	Hepatitis
ABP55566	Hepatitis
AAE32872	Hepatitis
AAE32877	Hepatitis
AAE32878	Hepatitis
AAE32873	Hepatitis
AAR58593	Hepatitis
ADL17784	Hepatitis
AAR96563	Hepatitis
AAR63349	Hepatitis
AAR96547	Hepatitis
AAR96534	Hepatitis
AAR67628	Non-A Non
AAR50076	NANBH vir
ADJ81681	Non-A non
AAR4088	NANBH hepa
AAR38280	NANBH hepa
AAR38282	NANBH hepa
AAR38281	NANBH hepa
AAR49832	Beat-gala
ADC42917	Hepatitis
ADX40795	HCV polym
ADX40792	HCV polym
ADX40826	HCV polym
AAB30733	Amino aci
AAB30731	Amino aci
AAB30730	Amino aci
AAB30732	Amino aci
ADX40827	HCV polym
ADX40822	HCV polym
AAR33214	NANBH vir
AAR33538	NANBH vir
AAR33539	NANBH vir
AAE59172	Protein e
AAE31168	Amino aci
AAB30729	Amino aci
ABG30688	Humán HCV
ADV04738	Hepatitis
ADX40787	HCV polym
ADX40815	HCV polym
ADX40819	HCV polym
ADX40778	HCV polym
AAR73111	Antigen f
AAR59125	Peptide f
AAR78946	HCV core
AAR78946	HCV core
AAR7652	Hepatitis
AAR91054	HCV-1 der
AAW39446	Human HCV
AAW54635	Peptide f
AAV10219	T cell ep
AAV10441	HLA Class
AAV73106	Hepatitis
AAJ03866	Hepatitis
AAJ03866	Hepatitis
AAJ01746	Hepatitis
AAJ03864	Hepatitis
AAJ00011	Hepatitis
AAJ00229	Hepatitis

98 42 89.4 9 4 AAJ03787 Aaj03787 Hepatitis
 99 42 89.4 9 4 AAJ04086 Aaj04086 Hepatitis
 100 42 89.4 9 5 ABG79901 Abg79901 MHC class

ALIGNMENTS

RESULT 1
 ID AAY82996 standard; peptide; 9 AA.
 XX
 AC AAY82996;
 XX
 DT 04-JUL-2000 (first entry)
 XX
 DE Substituted hepatitis C virus core polypeptide antigenic fragment.
 XX
 KW Hepatitis C virus; HCV; core polypeptide; antigen; epitope; agretope;
 KW anchor residue; cytotoxic T lymphocyte; CTL; immune response; MHC;
 KW Major histocompatibility complex; vaccine; treatment.
 XX
 OS Synthetic.
 OS Hepatitis C virus; (HCV).
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 8 /label= Ala substituted for Leu
 FT
 XX WO200011186-A1.
 XX
 PD 02-MAR-2000.
 XX
 XX 17-AUG-1999; 99WO-US018674.
 XX
 XX 21-AUG-1998; 98US-0097446P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Berzofsky JA, Sarobe P, Pendleton CD, Feinstein SM, Arichi T;
 XX Major ME;
 XX WPI; 2000-246569/21.
 XX
 XX Hepatitis C virus polypeptides is useful as a vaccine for treating
 XX Hepatitis C virus infection and for activating cytotoxic T lymphocytes.
 XX
 PS Claim 16; Page 71; 78pp; English.
 XX
 CC Peptide fragments of the Hepatitis C virus (HCV) core polypeptide can be
 CC used to elicit an immune response. A cytotoxic T-lymphocyte (CTL)
 CC response is present in patients acutely and chronically infected by HCV.
 CC CTL's recognise viral antigens as peptides presented by Class I molecules
 CC of the major histocompatibility complex (MHC). These peptide antigens are
 CC typically 8-10 amino acids long. These peptide antigens typically have a
 CC sequence pattern or motif depending upon which particular MHC antigen
 CC they are bound and presented by. The motifs are based on the presence in
 CC precise positions in the peptide sequence of several amino acids
 CC (agretopic residues) called anchor residues, responsible for interactions
 CC between peptide and MHC molecule, as well as other secondary position
 CC that may help to stabilise the interaction. Thus, single amino acid
 CC changes within the peptide sequence can enhance the immune response.
 CC Peptides derived from the HCV core polypeptide having substituted amino
 CC acids within their sequence, specifically a hepatitis C virus core
 CC polypeptide comprising an L to an A substitution at amino acid position
 CC 139 enhance the immune response against HCV. They can therefore be used
 CC as a vaccine or for treating HCV infection. This peptide is a fragment of
 CC the substituted HCV core polypeptide and comprises the region of amino
 CC acids within that polypeptide from position 132 to position 140 which
 CC contains the amino acid substitution
 XX
 XX Sequence 9 AA;

Query Match 100.0%; Score 47; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. NO. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DLMGYIPAV 9
 |||||
 Db 1 DLMGYIPAV 9

RESULT 2
 ID AAB82052 standard; peptide; 9 AA.
 XX
 AC AAB82052;
 XX
 DT 06-AUG-2003 (revised)
 DT 22-JUN-2001 (first entry)
 XX
 DE HCV antigen, core 132-140.
 XX
 KW Antigen; immunostimulant; vaccine; pharmaceutical composition; antiviral;
 KW viral infection.
 XX
 OS Hepatitis C virus.
 XX
 XX WO200124822-A2.
 XX
 PD 12-APR-2001.
 XX
 XX 02-OCT-2000; 2000WO-EP009657.
 XX
 XX 01-OCT-1999; 99AT-00001680.
 XX
 XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
 XX
 XX Fleitmann J, Mattner F, Buschle M, Melling J;
 XX WPI; 2001-290577/30.
 XX
 XX New pharmaceutical composition comprising an antigen, an
 XX immunostimulating substance and a polycationic polymer, useful in
 XX manufacturing vaccines.
 XX
 PS Claim 12; Page 16; 20pp; English.
 XX
 CC The present invention relates to a pharmaceutical composition comprising
 CC (a) an antigen; (b) an immunostimulating substance consisting of
 CC neuroactive compounds, hormones, compounds having growth hormone activity
 CC or their mixtures; and (c) a polycationic polymer. The present sequence
 CC is an antigenic peptide derived from Hepatitis C virus, which was used in
 CC the present invention. The composition is useful in manufacturing
 CC vaccines. (Updated on 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 47; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. NO. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DLMGYIPAV 9
 |||||
 Db 1 DLMGYIPAV 9

RESULT 3
 ID ADS97427 standard; peptide; 9 AA.
 XX
 AC ADS97427;
 XX
 DT 30-DEC-2004 (first entry)
 XX
 DE Hepatitis C virus-derived p87 peptide for improved vaccine.

XX virucide; anti-HIV; hepatotropic; antiinflammatory; vaccine;
 KW viral infection; antigen; immunostimulatory oligodeoxynucleic acid;
 KW influenza virus; HBV; HIV; HCV; HPV; JEV.
 XX Hepatitis C virus.
 OS WO2004084938-A1.
 XX 07-OCT-2004.
 XX 22-MAR-2004; 2004WO-EP003002.
 XX 24-MAR-2003; 2003EP-00450072.
 PR 11-APR-2003; 2003EP-00450084.
 PR 11-JUL-2003; 2003EP-00450171.
 XX (INTE-) INTERCELL AG.
 PA Buschle M, Habel A, Fritz J, Prinz K, Lingnau K;
 XX WPI; 2004-737255/72.
 XX Vaccine useful for preventing viral infections, comprises antigen,
 PT peptide and immunostimulatory oligodeoxynucleic acid molecule.
 PS Example 6; Page 27; 62pp; English.
 XX The invention relates to a vaccine (V1) for preventing viral infections
 CC comprises an antigen, a peptide comprising a sequence R1-XZXNZX-R2,
 CC where N is 3-7 (preferably 5); X is positively charged natural and/or non
 CC -natural amino acid residue; Z is amino acid residue chosen from Leu,
 CC Val, Ile, Phe and/or Trp; R1 and R2 is chosen from -H, -NH2, -COCH3, -
 CC COH, a peptide with up to 20 amino acid residues or peptide reactive
 CC group or peptide linker with or without peptide, and X-R2 may be an
 CC amide, ester or thioester of the C-terminal amino acid residue of the
 CC peptide (Peptide A); and an immunostimulatory oligodeoxynucleic acid
 CC molecule (ODN). (V1) is useful for preventing viral infections cost by
 CC influenza virus, HBV, HIV, HCV, HPV or JEV. A mixture of Peptide A and a
 CC I-/U-ODN (PI) is useful for improving the protective efficacy of (V1).
 CC This sequence corresponds to peptide p87 derived from hepatitis C virus
 CC protein and used in the vaccine of the invention to generate HCV-specific
 CC type 1 cellular response in mice.
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 47; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DLMGYIPAV 9
 Db |||||
 1 DLMGYIPAV 9
 RESULT 4
 ADV96878
 ID ADV96878 standard; peptide; 9 AA.
 XX
 AC ADV96878;
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE HCV-derived vaccine peptide p87 #1.
 XX
 KW Epitope mapping; vaccine; T-cell; Hepatitis C virus infection; infection;
 KW gastrointestinal disease; Virucide; Antiinflammatory; Hepatotropic.
 XX
 OS Hepatitis C virus.
 XX
 PN WO2005004910-A2.
 XX 20-JAN-2005.
 PD

XX 09-JUL-2004; 2004WO-EP007540.
 PF 11-JUL-2003; 2003EP-00450171.
 PR 12-MAR-2004; 2004EP-00450062.
 XX (INTE-) INTERCELL AG.
 XX Buschle M, Frisch J, Klade C, Lingnau K, Zauner W, Zettlmeissl G;
 PI WPI; 2005-101792/11.
 DR
 XX Hepatitis C virus HCV vaccine useful for preparation of medicament for
 PT prevention and treatment of infection with HCV, comprises two epitopes
 PT from different hotspot epitope containing specific peptide.
 XX Example 4; Page 33; 59pp; English.
 PS The invention relates to a Hepatitis C virus (HCV) vaccine (VA)
 CC comprising at least two epitopes, each from a different hotspot epitope,
 CC where a hotspot epitope is defined as an epitope containing peptide
 CC having specific sequences. Also included is the preparation of VA
 CC involving chemically synthesizing the two epitopes of VA, solubilizing
 CC the epitopes by an aqueous solution containing an organic acid chosen
 CC from formic acid, acetic acid, propionic acid, butyric acid and its
 CC halogenated or hydroxylated forms, mixing the solubilized epitopes and
 CC optionally lyophilizing the mixed epitopes. The vaccine is useful for the
 CC preparation of a medicament for the prevention and treatment of an
 CC infection with HCV. The present sequence is an HCV epitope peptide
 CC derived from a hotspot epitope, used as a vaccine.
 XX Sequence 9 AA;
 SQ Query Match 100.0%; Score 47; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DLMGYIPAV 9
 Db |||||
 1 DLMGYIPAV 9
 RESULT 5
 ADV96796
 ID ADV96796 standard; peptide; 9 AA.
 XX
 AC ADV96796;
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE HCV T-cell epitope peptide 87 #1.
 XX
 KW Epitope mapping; vaccine; T-cell; Hepatitis C virus infection; infection;
 KW gastrointestinal disease; Virucide; Antiinflammatory; Hepatotropic.
 XX
 OS Hepatitis C virus.
 XX
 PN WO2005004910-A2.
 XX 20-JAN-2005.
 PD
 XX 09-JUL-2004; 2004WO-EP007540.
 PF 11-JUL-2003; 2003EP-00450171.
 PR 12-MAR-2004; 2004EP-00450062.
 XX (INTE-) INTERCELL AG.
 PA Buschle M, Frisch J, Klade C, Lingnau K, Zauner W, Zettlmeissl G;
 XX WPI; 2005-101792/11.
 DR
 XX Hepatitis C virus HCV vaccine useful for preparation of medicament for

PT prevention and treatment of infection with HCV, comprises two epitopes
 PT from different hotspot epitope containing specific peptide.

XX Claim 5; Page 52; 59pp; English.

XX The invention relates to a Hepatitis C virus (HCV) vaccine (VA)
 CC comprising at least two epitopes, each from a different hotspot epitope,
 CC where a hotspot epitope is defined as an epitope containing peptide
 CC having specific sequences. Also included is the preparation of VA,
 CC involving chemically synthesizing the two epitopes of VA, solubilizing
 CC the epitopes by an aqueous solution containing an organic acid chosen
 CC from formic acid, acetic acid, propionic acid, butyric acid and its
 CC halogenated or hydroxylated forms, mixing the solubilized epitopes and
 CC optionally lyophilizing the mixed epitopes. The vaccine is useful for the
 CC preparation of a medicament for the prevention and treatment of an
 CC infection with HCV. The present sequence is an HCV epitope peptide
 CC derived from a hotspot epitope, used as a vaccine.

XX Sequence 9 AA;

Query Match 100.0%; Score 47; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9

Db 1 DLMGYIPAV 9

RESULT 6

ADV96890
 ID ADV96890 standard; peptide; 9 AA.

XX AC ADV96890;

XX DT 07-APR-2005 (first entry)

XX DE HCV-derived peptide binding HLA class I and/or II, 87 #1.

XX Epitope mapping; vaccine; T-cell; Hepatitis C virus infection; infection;
 XX gastrointestinal disease; Virucide; Antiinflammatory; Hepatotropic.

XX OS Hepatitis C virus.

XX WO2005004910-A2.

XX PD 20-JAN-2005.

XX PF 09-JUL-2004; 2004WO-EP007540.

XX PR 11-JUL-2003; 2003EP-00450171.

XX PR 12-MAR-2004; 2004EP-00450062.

XX PA (INTE-) INTERCELL AG.

XX PI Buschle M, Frisch J, Klade C, Lingnau K, Zauner W, Zettlmeissl G;

XX WIPI; 2005-101792/11.

XX Hepatitis C virus HCV vaccine useful for preparation of medicament for
 PT prevention and treatment of infection with HCV, comprises two epitopes
 PT from different hotspot epitope containing specific peptide.

XX Example 5; Page 35; 59pp; English.

XX The invention relates to a Hepatitis C virus (HCV) vaccine (VA)
 CC comprising at least two epitopes, each from a different hotspot epitope,
 CC where a hotspot epitope is defined as an epitope containing peptide
 CC having specific sequences. Also included is the preparation of VA,
 CC involving chemically synthesizing the two epitopes of VA, solubilizing
 CC the epitopes by an aqueous solution containing an organic acid chosen
 CC from formic acid, acetic acid, propionic acid, butyric acid and its
 CC halogenated or hydroxylated forms, mixing the solubilized epitopes and

CC optionally lyophilizing the mixed epitopes. The vaccine is useful for the
 CC preparation of a medicament for the prevention and treatment of an
 CC infection with HCV. The present sequence is an HCV epitope peptide
 CC derived from a hotspot epitope, used as a vaccine.

XX Sequence 9 AA;

Query Match 100.0%; Score 47; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9

Db 1 DLMGYIPAV 9

RESULT 7

ADV96886
 ID ADV96886 standard; peptide; 9 AA.

XX AC ADV96886;

XX DT 07-APR-2005 (first entry)

XX DE HCV-derived vaccine peptide p87 #2.

XX Epitope mapping; vaccine; T-cell; Hepatitis C virus infection; infection;
 XX gastrointestinal disease; Virucide; Antiinflammatory; Hepatotropic.

XX OS Hepatitis C virus.

XX WO2005004910-A2.

XX PD 20-JAN-2005.

XX PF 09-JUL-2004; 2004WO-EP007540.

XX PR 11-JUL-2003; 2003EP-00450171.

XX PR 12-MAR-2004; 2004EP-00450062.

XX PA (INTE-) INTERCELL AG.

XX PI Buschle M, Frisch J, Klade C, Lingnau K, Zauner W, Zettlmeissl G;

XX WIPI; 2005-101792/11.

XX Hepatitis C virus HCV vaccine useful for preparation of medicament for
 PT prevention and treatment of infection with HCV, comprises two epitopes
 PT from different hotspot epitope containing specific peptide.

XX Example 5; Page 35; 59pp; English.

XX The invention relates to a Hepatitis C virus (HCV) vaccine (VA)
 CC comprising at least two epitopes, each from a different hotspot epitope,
 CC where a hotspot epitope is defined as an epitope containing peptide
 CC having specific sequences. Also included is the preparation of VA,
 CC involving chemically synthesizing the two epitopes of VA, solubilizing
 CC the epitopes by an aqueous solution containing an organic acid chosen
 CC from formic acid, acetic acid, propionic acid, butyric acid and its
 CC halogenated or hydroxylated forms, mixing the solubilized epitopes and
 CC optionally lyophilizing the mixed epitopes. The vaccine is useful for the
 CC preparation of a medicament for the prevention and treatment of an
 CC infection with HCV. The present sequence is an HCV epitope peptide
 CC derived from a hotspot epitope, used as a vaccine.

XX Sequence 9 AA;

Query Match 100.0%; Score 47; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9

Db 1 DLMGYIPAV 9

```

Db      1 DLMGYIPAV 9

RESULT 8
ADV96961
ID ADV96961 standard; peptide; 9 AA.
XX AC ADV96961;
XX DT 07-APR-2005 (first entry)
XX DE HCV-derived vaccine peptide 87.
XX KW Epitope mapping; vaccine; T-cell; Hepatitis C virus infection; infection;
XX KW gastrointestinal disease; Virucide; Antiinflammatory; Hepatotropic.
XX OS Hepatitis C virus.
XX PN WO2005004910-A2.
XX PD 20-JAN-2005.
XX PF 09-JUL-2004; 2004WO-EP007540.
XX PR 11-JUL-2003; 2003EP-00450171.
XX PR 12-MAR-2004; 2004EP-00450062.
XX PA (INTE-) INTERCELL AG.
XX PI Buschle M, Frisch J, Klade C, Lingnau K, Zauner W, Zettlmeissl G;
XX PF WPI; 2005-101792/11.
XX PR Hepatitis C virus HCV vaccine useful for preparation of medicament for
XX PR prevention and treatment of infection with HCV, comprises two epitopes
XX PR from different hotspot epitope containing specific peptide.
XX PS Example 5; Page 37; 59pp; English.
XX CC The invention relates to a Hepatitis C virus (HCV) vaccine (VA)
XX CC comprising at least two epitopes, each from a different hotspot epitope,
XX CC where a hotspot epitope is defined as an epitope containing peptide
XX CC having specific sequences. Also included is the preparation of VA,
XX CC involving chemically synthesizing the two epitopes of VA, solubilizing
XX CC the epitopes by an aqueous solution containing an organic acid chosen
XX CC from formic acid, acetic acid, propionic acid, butyric acid and its
XX CC halogenated or hydroxylated forms, mixing the solubilized epitopes and
XX CC optionally lyophilizing the mixed epitopes. The vaccine is useful for the
XX CC preparation of a medicament for the prevention and treatment of an
XX CC infection with HCV. The present sequence is an HCV epitope peptide
XX CC derived from a hotspot epitope, used as a vaccine.
XX SQ Sequence 9 AA;

Query Match      100.0%; Score 47; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DLMGYIPAV 9
        |||||
Db      1 DLMGYIPAV 9
        |||||

RESULT 10
ADV96917
ID ADV96917 standard; peptide; 9 AA.
XX AC ADV96917;
XX DT 07-APR-2005 (first entry)
XX DE HCV-derived peptide binding HLA clas I and/or II, 87 #3.
XX KW Epitope mapping; vaccine; T-cell; Hepatitis C virus infection; infection;
XX KW gastrointestinal disease; Virucide; Antiinflammatory; Hepatotropic.
XX OS Hepatitis C virus.
XX PN WO2005004910-A2.
XX PD 20-JAN-2005.
XX PF 09-JUL-2004; 2004WO-EP007540.
XX PR 11-JUL-2003; 2003EP-00450171.
XX PR 12-MAR-2004; 2004EP-00450062.

```

```

Db      1 DLMGYIPAV 9

RESULT 8
ADV96961
ID ADV96961 standard; peptide; 9 AA.
XX AC ADV96961;
XX DT 07-APR-2005 (first entry)
XX DE HCV-derived vaccine peptide 87.
XX KW Epitope mapping; vaccine; T-cell; Hepatitis C virus infection; infection;
XX KW gastrointestinal disease; Virucide; Antiinflammatory; Hepatotropic.
XX OS Hepatitis C virus.
XX PN WO2005004910-A2.
XX PD 20-JAN-2005.
XX PF 09-JUL-2004; 2004WO-EP007540.
XX PR 11-JUL-2003; 2003EP-00450171.
XX PR 12-MAR-2004; 2004EP-00450062.
XX PA (INTE-) INTERCELL AG.
XX PI Buschle M, Frisch J, Klade C, Lingnau K, Zauner W, Zettlmeissl G;
XX PF WPI; 2005-101792/11.
XX PR Hepatitis C virus HCV vaccine useful for preparation of medicament for
XX PR prevention and treatment of infection with HCV, comprises two epitopes
XX PR from different hotspot epitope containing specific peptide.
XX PS Example 6; Page 40; 59pp; English.
XX CC The invention relates to a Hepatitis C virus (HCV) vaccine (VA)
XX CC comprising at least two epitopes, each from a different hotspot epitope,
XX CC where a hotspot epitope is defined as an epitope containing peptide
XX CC having specific sequences. Also included is the preparation of VA,
XX CC involving chemically synthesizing the two epitopes of VA, solubilizing
XX CC the epitopes by an aqueous solution containing an organic acid chosen
XX CC from formic acid, acetic acid, propionic acid, butyric acid and its
XX CC halogenated or hydroxylated forms, mixing the solubilized epitopes and
XX CC optionally lyophilizing the mixed epitopes. The vaccine is useful for the
XX CC preparation of a medicament for the prevention and treatment of an
XX CC infection with HCV. The present sequence is an HCV epitope peptide
XX CC derived from a hotspot epitope, used as a vaccine.
XX SQ Sequence 9 AA;

Query Match      100.0%; Score 47; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DLMGYIPAV 9
        |||||
Db      1 DLMGYIPAV 9
        |||||

RESULT 9
ADV96912
ID ADV96912 standard; peptide; 9 AA.
XX AC ADV96912;
XX DT 07-APR-2005 (first entry)
XX DE HCV-derived peptide binding HLA clas I and/or II, 87 #2.

```



```

CC vaccine. This sequence represents a Ty-2 associated peptide.
XX
SQ Sequence 9 AA;

Query Match          91.5%; Score 43; DB 8; Length 9;
Best Local Similarity 88.9%; Pred. No. 28+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
   |||||
DB 1 DLMGYIPV 9

RESULT 13
ADV96979
ID ADV96979 standard; peptide; 13 AA.
XX
AC ADV96979;
XX
DT 07-APR-2005 (first entry)
XX
DE HCV T-cell epitope hotspot peptide #1.
XX
KW Epitope mapping; vaccine; T-cell; Hepatitis C virus infection; infection;
KW gastrointestinal disease; virucide; Antiinflammatory; Hepatotropic.
XX
OS Hepatitis C virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 8 /label= Ala, Leu
XX
FN WO2005004910-A2.
XX
PD 20-JAN-2005.
XX
PF 09-JUL-2004; 2004WO-EP007540.
XX
PR 11-JUL-2003; 2003EP-00450171.
XX
PR 12-MAR-2004; 2004EP-00450062.
XX
PA (INTE-) INTERCELL AG.
XX
PI Buschle M, Frisch J, Klade C, Lingnau K, Zauner W, Zettlmeisl G;
XX
DR WPI; 2005-101792/11.
XX
PT Hepatitis C virus HCV vaccine useful for preparation of medicament for
PT prevention and treatment of infection with HCV, comprises two epitopes
PT from different hotspot epitope containing specific peptide.
XX
PS Claim 1; Page 51; 59pp; English.
XX
CC The invention relates to a Hepatitis C virus (HCV) vaccine (VA)
CC comprising at least two epitopes, each from a different hotspot epitope,
CC where a hotspot epitope is defined as an epitope containing peptide
CC having specific sequences. Also included is the preparation of VA,
CC involving chemically synthesizing the two epitopes of VA, solubilizing
CC the epitopes by an aqueous solution containing an organic acid chosen
CC from formic acid, acetic acid, propionic acid, butyric acid and its
CC halogenated or hydroxylated forms, mixing the solubilized epitopes and
CC optionally lyophilizing the mixed epitopes. The vaccine is useful for the
CC preparation of a medicament for the prevention and treatment of an
CC infection with HCV. The present sequence is an HCV hotspot epitope.
XX
SQ Sequence 13 AA;

Query Match          91.5%; Score 43; DB 9; Length 13;
Best Local Similarity 88.9%; Pred. No. 0.093;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
   |||||

CC vaccine. This sequence represents a Ty-2 associated peptide.
XX
SQ Sequence 9 AA;

Query Match          91.5%; Score 43; DB 8; Length 9;
Best Local Similarity 88.9%; Pred. No. 28+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
   |||||
DB 1 DLMGYIPV 9

RESULT 14
ADL25899
ID ADL25899 standard; peptide; 15 AA.
XX
AC ADL25899;
XX
DT 17-JUN-2004 (first entry)
XX
DE Synthetic peptide A86 derived from a conserved region of HCV.
XX
KW HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;
KW major histocompatibility complex; human leukocyte antigen.
XX
OS Synthetic.
XX
FN WO2004024182-A2.
XX
PD 25-MAR-2004.
XX
PF 27-AUG-2003; 2003WO-EP009482.
XX
PR 13-SEP-2002; 2002AT-00001376.
XX
PR 27-FEB-2003; 2003WO-EP002005.
XX
PR 11-JUL-2003; 2003EP-00450171.
XX
PA (INTE-) INTERCELL AG.
XX
PI Buschle M, Habel A, Klade C, Mattner F, Otava O, Vytvytska O;
XX
PI Zauner W, Zinke S, Kirlappos H;
XX
DR WPI; 2004-269899/25.
XX
PT Isolating Hepatitis C Virus peptides (Hps) which have a binding capacity
PT to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
PT molecule by separating the complex from the HCV-peptides which do not
PT bind to the molecule.
XX
PS Example 1; Page 30; 73pp; English.
XX
CC The invention relates to a novel method for isolating Hepatitis C Virus
CC (HCV) peptides (Hps). The method of the invention has virucide activity,
CC and may be useful in producing a vaccine. The method is useful for
CC isolating Hepatitis C Virus peptides (Hps) which have a binding capacity
CC to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
CC MHC/HLA molecule for preparing a vaccine against HCV infection. The
CC cells, a T cell clone or a T cell population or preparation is useful for
CC identifying heteroclitic epitopes or for preparing a composition for
CC treating HCV infection. The present sequence represents a synthetic
CC peptide derived from a conserved region of HCV.
XX
SQ Sequence 15 AA;

Query Match          91.5%; Score 43; DB 8; Length 15;
Best Local Similarity 88.9%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
   |||||
DB 7 DLMGYIPV 15

RESULT 15
ADL25904
ID ADL25904 standard; peptide; 15 AA.
XX
AC ADL25904;
XX
DT 17-JUN-2004 (first entry)
XX
DE Synthetic peptide A91 derived from a conserved region of HCV.

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XX KW HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;
XX KW major histocompatibility complex; human leukocyte antigen.
XX OS Synthetic.
XX PN WO2004024182-A2.
XX PD 25-MAR-2004.
XX PF 27-AUG-2003; 2003WO-EP009482.
XX PR 13-SEP-2002; 2002AT-00001376.
XX PR 27-FEB-2003; 2003WO-EP002005.
XX PR 11-JUL-2003; 2003EP-00450171.
XX PA (INTE-) INTERCELL AG.
XX PI Buschle M, Habel A, Klade C, Mattner F, Otava O, Vytvytska O;
XX PI Zauner W, Zinke S, Kiriappos H;
XX DR WPI; 2004-269899/25.
XX PT Isolating Hepatitis C Virus peptides (HPs) which have a binding capacity
XX PT to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
XX PT molecule by separating the complex from the HCV-peptides which do not
XX PT bind to the molecule.
XX PS Example 1; Page 30; 73pp; English.
XX CC The invention relates to a novel method for isolating Hepatitis C Virus
XX CC (HCV) peptides (HPs). The method of the invention has virucide activity,
XX CC and may be useful in producing a vaccine. The method is useful for
XX CC isolating Hepatitis C Virus peptides (HPs) which have a binding capacity
XX CC to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
XX CC MHC/HLA molecule for preparing a vaccine against HCV infection. The T
XX CC cells, a T cell clone or a T cell population or preparation is useful for
XX CC identifying heteroclitic epitopes or for preparing a composition for
XX CC treating HCV infection. The present sequence represents a synthetic
XX CC peptide derived from a conserved region of HCV.
XX SQ Sequence 15 AA;
XX
XX Query Match 91.5%; Score 43; DB 8; Length 15;
XX Best Local Similarity 88.9%; Pred. No. 0.11;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 DLMGYIPAV 9
XX DB 2 DLMGYIPVV 10
XX
XX RESULT 16
XX ADL25905
XX ID ADL25905 standard; peptide; 15 AA.
XX AC ADL25905;
XX XX
XX DT 17-JUN-2004 (first entry)
XX DE Synthetic peptide A92 derived from a conserved region of HCV.
XX KW HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;
XX KW major histocompatibility complex; human leukocyte antigen.
XX OS Synthetic.
XX PN WO2004024182-A2.
XX PD 25-MAR-2004.
XX PF 27-AUG-2003; 2003WO-EP009482.
XX PR 13-SEP-2002; 2002AT-00001376.
XX PR 27-FEB-2003; 2003WO-EP002005.
XX PR 11-JUL-2003; 2003EP-00450171.
XX PA (INTE-) INTERCELL AG.
XX PI Buschle M, Habel A, Klade C, Mattner F, Otava O, Vytvytska O;
XX PI Zauner W, Zinke S, Kiriappos H;
XX DR WPI; 2004-269899/25.
XX PT Isolating Hepatitis C Virus peptides (HPs) which have a binding capacity
XX
PR 13-SEP-2002; 2002AT-00001376.
PR 27-FEB-2003; 2003WO-EP002005.
PR 11-JUL-2003; 2003EP-00450171.
PR PA (INTE-) INTERCELL AG.
PR PI Buschle M, Habel A, Klade C, Mattner F, Otava O, Vytvytska O;
PR PI Zauner W, Zinke S, Kiriappos H;
PR DR WPI; 2004-269899/25.
PR PT Isolating Hepatitis C Virus peptides (HPs) which have a binding capacity
PR

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PT to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 PT molecule by separating the complex from the HCV-peptides which do not
 bind to the molecule.

PS Example 1; Page 30; 73pp; English.

XX The invention relates to a novel method for isolating Hepatitis C Virus
 CC (HCV) peptides (Hps). The method of the invention has virucide activity,
 CC and may be useful in producing a vaccine. The method is useful for
 CC isolating Hepatitis C Virus peptides (Hps) which have a binding capacity
 CC to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 CC MHC/HLA molecule or a complex comprising the HCV-peptide and the
 CC cells, a T cell clone or a T cell population or preparation is useful for
 CC identifying heteroclitic epitopes or for preparing a composition for
 CC treating HCV infection. The present sequence represents a synthetic
 CC peptide derived from a conserved region of HCV.

XX Sequence 15 AA;

Query Match 91.5%; Score 43; DB 8; Length 15;
 Best Local Similarity 88.9%; Pred. No. 0.11;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
 Db 6 DLMGYIPV 14
 |||||

RESULT 18

ADL25901
 ID ADL25901 standard; peptide; 15 AA.

XX ADL25901;

DT 17-JUN-2004 (first entry)

XX Synthetic peptide A88 derived from a conserved region of HCV.

XX HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;
 KW major histocompatibility complex; human leukocyte antigen.

XX Synthetic.

XX WO2004024182-A2.

XX 25-MAR-2004.

XX 27-AUG-2003; 2003WO-EP009482.

XX 13-SEP-2002; 2002AT-00001376.

XX 27-FEB-2003; 2003WO-EP002005.

XX 11-JUL-2003; 2003EP-00450171.

XX (INTE-) INTERCELL AG.

XX Buschle M, Habel A, Klade C, Mattner F, Otava O, Vytvytska O;

PI Zauner W, Zinke S, Kiriappos H;

XX WPI; 2004-269899/25.

XX Isolating Hepatitis C Virus peptides (Hps) which have a binding capacity
 PT to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 PT molecule by separating the complex from the HCV-peptides which do not
 PT bind to the molecule.

XX Example 1; Page 30; 73pp; English.

XX The invention relates to a novel method for isolating Hepatitis C Virus
 CC (HCV) peptides (Hps). The method of the invention has virucide activity,
 CC and may be useful in producing a vaccine. The method is useful for
 CC isolating Hepatitis C Virus peptides (Hps) which have a binding capacity
 CC to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 CC MHC/HLA molecule for preparing a vaccine against HCV infection. The T

CC cells, a T cell clone or a T cell population or preparation is useful for
 CC identifying heteroclitic epitopes or for preparing a composition for
 CC treating HCV infection. The present sequence represents a synthetic
 CC peptide derived from a conserved region of HCV.

XX Sequence 15 AA;

Query Match 91.5%; Score 43; DB 8; Length 15;
 Best Local Similarity 88.9%; Pred. No. 0.11;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
 Db 5 DLMGYIPV 13
 |||||

RESULT 19

ADL25903

ID ADL25903 standard; peptide; 15 AA.

XX ADL25903;

DT 17-JUN-2004 (first entry)

XX Synthetic peptide A90 derived from a conserved region of HCV.

XX HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;
 KW major histocompatibility complex; human leukocyte antigen.

XX Synthetic.

XX WO2004024182-A2.

XX 25-MAR-2004.

XX 27-AUG-2003; 2003WO-EP009482.

XX 13-SEP-2002; 2002AT-00001376.

XX 27-FEB-2003; 2003WO-EP002005.

XX 11-JUL-2003; 2003EP-00450171.

XX (INTE-) INTERCELL AG.

XX Buschle M, Habel A, Klade C, Mattner F, Otava O, Vytvytska O;

PI Zauner W, Zinke S, Kiriappos H;

XX WPI; 2004-269899/25.

XX Isolating Hepatitis C Virus peptides (Hps) which have a binding capacity
 PT to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 PT molecule by separating the complex from the HCV-peptides which do not
 PT bind to the molecule.

XX Example 1; Page 30; 73pp; English.

XX The invention relates to a novel method for isolating Hepatitis C Virus
 CC (HCV) peptides (Hps). The method of the invention has virucide activity,
 CC and may be useful in producing a vaccine. The method is useful for
 CC isolating Hepatitis C Virus peptides (Hps) which have a binding capacity
 CC to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 CC MHC/HLA molecule for preparing a vaccine against HCV infection. The T
 CC cells, a T cell clone or a T cell population or preparation is useful for
 CC identifying heteroclitic epitopes or for preparing a composition for
 CC treating HCV infection. The present sequence represents a synthetic
 CC peptide derived from a conserved region of HCV.

XX Sequence 15 AA;

Query Match 91.5%; Score 43; DB 8; Length 15;
 Best Local Similarity 88.9%; Pred. No. 0.11;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9

```

DE      Synthetic peptide 1649 derived from a conserved region of HCV.
XX
XX      HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;
KW      major histocompatibility complex; human leukocyte antigen.
XX
XX      Synthetic.
OS
XX      WO2004024182-A2.
XX
XX      25-MAR-2004.
PD
XX
XX      27-AUG-2003; 2003WO-EP009482.
XX
XX      13-SEP-2002; 2002AT-00001376.
XX
XX      27-FEB-2003; 2003WO-EP002005.
PR
XX      11-JUL-2003; 2003EP-00450171.
XX
XX      (INTE-) INTERCELL AG.
PA
XX      Buschle M, Habel A, Klade C, Mattner F, Otava O, Vytvytska O;
PI      Zauner W, Zinke S, Kiriappos H;
XX
XX      WPI; 2004-269899/25.
XX
XX      Isolating Hepatitis C Virus peptides (Hps) which have a binding capacity
XX      to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
XX      molecule by separating the complex from the HCV-peptides which do not
XX      bind to the molecule.
XX
XX      Example 1; Page 32; 73pp; English.
XX
XX      The invention relates to a novel method for isolating Hepatitis C Virus
XX      (HCV) peptides (Hps). The method of the invention has virucide activity,
XX      and may be useful in producing a vaccine. The method is useful for
XX      isolating Hepatitis C Virus peptides (Hps) which have a binding capacity
XX      to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
XX      MHC/HLA molecule for preparing a vaccine against HCV infection. The T
XX      cells, a T cell clone or a T cell population or preparation is useful for
XX      identifying heteroclitic epitopes or for preparing a composition for
XX      treating HCV infection. The present sequence represents a synthetic
XX      peptide derived from a conserved region of HCV.
XX
XX      Sequence 36 AA;
SQ
XX
XX      Query Match      91.5%; Score 43; DB 8; Length 36;
XX      Best Local Similarity 88.9%; Pred. No. 0.29;
XX      Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX      QY      1 DLMGYIPAV 9
XX      Db      22 DLMGYIPV 30
XX
XX      RESULT 22
XX      AAR52735
XX      ID AAR52735 standard; protein; 168 AA.
XX
XX      AC AAR52735;
XX
XX      DT 31-JAN-1995 (first entry)
XX
XX      DE HCV antigen.
XX
XX      KW Hepatitis C virus; HCV; antigen; diagnosis; reagent; agglutination.
XX
XX      OS Synthetic.
XX
XX      PN JP06102273-A.
XX
XX      PD 15-APR-1994.
XX
XX      PF 18-SEP-1992; 92JP-00250027.
XX
XX

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Db      3 DLMGYIPV 11
XX
XX      RESULT 20
XX      ADL25902
XX      ID ADL25902 standard; peptide; 15 AA.
XX
XX      AC ADL25902;
XX
XX      DT 17-JUN-2004 (first entry)
XX
XX      DE Synthetic peptide A89 derived from a conserved region of HCV.
XX
XX      KW HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;
XX      major histocompatibility complex; human leukocyte antigen.
XX
XX      OS Synthetic.
XX
XX      PN WO2004024182-A2.
XX
XX      PD 25-MAR-2004.
XX
XX      PF 27-AUG-2003; 2003WO-EP009482.
XX
XX      PR 13-SEP-2002; 2002AT-00001376.
XX
XX      PR 27-FEB-2003; 2003WO-EP002005.
XX
XX      PR 11-JUL-2003; 2003EP-00450171.
XX
XX      (INTE-) INTERCELL AG.
PA
XX      Buschle M, Habel A, Klade C, Mattner F, Otava O, Vytvytska O;
PI      Zauner W, Zinke S, Kiriappos H;
XX
XX      WPI; 2004-269899/25.
XX
XX      Isolating Hepatitis C Virus peptides (Hps) which have a binding capacity
XX      to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
XX      molecule by separating the complex from the HCV-peptides which do not
XX      bind to the molecule.
XX
XX      Example 1; Page 30; 73pp; English.
XX
XX      The invention relates to a novel method for isolating Hepatitis C Virus
XX      (HCV) peptides (Hps). The method of the invention has virucide activity,
XX      and may be useful in producing a vaccine. The method is useful for
XX      isolating Hepatitis C Virus peptides (Hps) which have a binding capacity
XX      to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
XX      MHC/HLA molecule for preparing a vaccine against HCV infection. The T
XX      cells, a T cell clone or a T cell population or preparation is useful for
XX      identifying heteroclitic epitopes or for preparing a composition for
XX      treating HCV infection. The present sequence represents a synthetic
XX      peptide derived from a conserved region of HCV.
XX
XX      Sequence 15 AA;
SQ
XX
XX      Query Match      91.5%; Score 43; DB 8; Length 15;
XX      Best Local Similarity 88.9%; Pred. No. 0.11;
XX      Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX      QY      1 DLMGYIPAV 9
XX      Db      4 DLMGYIPV 12
XX
XX      RESULT 21
XX      ADL26466
XX      ID ADL26466 standard; peptide; 36 AA.
XX
XX      AC ADL26466;
XX
XX      DT 17-JUN-2004 (first entry)
XX
XX

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PR 18-SEP-1992; 92JP-00250027.
XX (TOKU ) TOKUYAMA SODA KK.
XX WPI; 1994-161280/20.
DR N-PSDB; AAQ62688.
XX
PT Immunological agglutination reagent for the diagnosis of hepatitis C -
PT comprising hepatitis C virus antigen polypeptide.
XX
PS Claim 2-3; Page 15-16; 18pp; Japanese.
XX
CC An new immunological agglutination reaction reagent for the diagnosis of
CC hepatitis C uses a HCV antigen polypeptide subjected to heat-treatment.
CC The HCV antigen active polypeptide contains one of the polypeptides given
CC in AAR52735-38
XX
SQ Sequence 168 AA;

Query Match 91.5%; Score 43; DB 2; Length 168;
Best Local Similarity 88.9%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 132 DLMGYIPVV 140

RESULT 23
AAR49831
ID AAR49831 standard; protein; 168 AA.
XX
AC AAR49831;
XX
DT 17-OCT-1994 (first entry)
XX
DE Antigenic fragment of hepatitis C virus.
XX
KW Hepatitis C virus; HCV; detection; infection; fusion protein; antibody;
KW fermentation; antigen.
XX
OS Hepatitis C virus.
XX
FN JP06046872-A.
XX
PD 22-FEB-1994.
XX
PF 24-JUL-1992; 92JP-00198806.
XX
PR 24-JUL-1992; 92JP-00198806.
XX
PA (TOKU ) TOKUYAMA SODA KK.
XX
DR WPI; 1994-097028/12.
DR N-PSDB; AAR49831.
XX
PT HCV antigen active fusion polypeptide - for the detection of anti-HCV
PT antibodies.
XX
PS Claim 1; Page 9; 15pp; Japanese.
XX
CC The polypeptide provokes an antibody response to hepatitis C virus (HCV).
CC It can be produced in large quantities by fusing this coding sequence to
CC the beta-galactosidase gene and then transforming E. coli with the
CC resulting construct. The E. coli can then be cultured and the fusion
CC protein expressed and recovered from the supernatant. The polypeptide
CC reacts specifically with anti-HCV antibodies and can be used for the
CC identification of such. It can therefore be used to identify individuals
CC infected with HCV
XX
SQ Sequence 168 AA;

Query Match 91.5%; Score 43; DB 2; Length 168;

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Best Local Similarity 88.9%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 132 DLMGYIPVV 140

RESULT 24
AAW41753
ID AAW41753 standard; protein; 188 AA.
XX
AC AAW41753;
XX
DT 22-MAY-1998 (first entry)
XX
DE Hepatitis C virus antigen.
XX
KW non-A non-B hepatitis virus; NANBH; hepatitis C virus; HCV; antigen;
KW diagnosis; detection.
XX
OS Hepatitis virus.
XX
FN JP05176774-A.
XX
PD 20-JUL-1993.
XX
PF 18-DEC-1991; 91JP-00354708.
XX
PR 18-DEC-1990; 90JP-00412020.
XX
PA (SHIM/) SHIMOTONO K.
PA (GREC ) GREEN CROSS CORP.
XX
DR WPI; 1993-260858/33.
XX
PT Protein contg. non-A non-B hepatitis antigen fragment - prepd. by
PT culturing transformants transformed by vector contg. base sequence coding
PT specified aminoacid sequences, used for detecting hepatitis.
XX
PS Claim 1; Fig 19; 53pp; Japanese.
XX
CC The present sequence is a non-A non-B hepatitis virus (NANBH) or
CC hepatitis C virus (HCV) antigen, useful for diagnosis or detection
XX
SQ Sequence 188 AA;

Query Match 91.5%; Score 43; DB 2; Length 188;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 140 DLMGYIPVV 148

RESULT 25
AAB71257
ID AAB71257 standard; protein; 190 AA.
XX
AC AAB71257;
XX
DT 06-AUG-2003 (revised)
DT 18-NOV-2002 (first entry)
XX
DE HCV type 2 capsid protein fragment.
XX
KW Capsid protein; attenuated vaccine; virucide; antiinflammatory;
KW hepatotropic; yellow fever; Japanese encephalitis; dengue;
KW classical swine fever; bovine viral diarrhoea; hepatitis C.
XX
OS Hepatitis C virus.
XX

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PN WO200266621-A1.
XX
PD 29-AUG-2002.
XX
XX PF 11-FEB-2002; 2002WO-AT000046.
XX
XX PR 21-FEB-2001; 2001AT-0000272.
XX
XX PA (HEINZ) HEINZ F X.
XX (MAND/) MANDL C.
XX
XX PI Heinz FX, Mandl C;
XX
XX WPI; 2002-667064/71.
XX
XX PT Attenuated flavivirus live vaccine, useful for protection against e.g.
XX yellow fever, comprises virus with attenuating deletion of amino acids
XX from the capsid protein.
XX
XX PS Disclosure; Fig 2; 30pp; German.
XX
XX CC This invention describes a novel attenuated flavivirus live vaccine
XX comprising a flavivirus mutant that has a deletion of at least 4
XX consecutive amino acids from the capsid protein, provided that the C-
XX terminal hydrophobic region is not affected by the deletion. The vaccine
XX of the invention has virucide, antiinflammatory and hepatotropic activity.
XX The attenuated vaccine, and similar nucleic acid vaccines that encode the
XX mutated capsid protein, are useful for protection against a wide range of
XX flavivirus diseases, e.g. yellow fever, Japanese encephalitis, dengue,
XX classical swine fever, bovine viral diarrhoea and hepatitis C. The
XX specified deletion: (i) produces a reliably attenuated virus that does
XX not revert to virulence; (ii) is exactly defined and does not effect
XX immune responses to important proteins; and (iii) can not generate a non-
XX natural virus by recombination. The mutant viruses eliminate the need to
XX produce large amounts of infectious/virulent viruses, and can be produced
XX with less expense. The protective response to flavivirus lasts
XX significantly longer than that to killed vaccines. This sequence
XX represents a fragment of the capsid protein from Hepatitis C virus (HCV)
XX type 1 described in the disclosure of the invention. (Updated on 06-AUG-
XX 2003 to correct OS field.)
XX
XX SQ Sequence 190 AA;
XX
XX Query Match 91.5%; Score 43; DB 5; Length 190;
XX Best Local Similarity 88.9%; Pred. No. 1.8;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 DLMGYIPAV 9
XX |||||
XX Db 131 DLMGYIPV 139
XX
XX RESULT 26
XX AAR92960
XX ID AAR92960 standard; protein; 191 AA.
XX
XX AC AAR92960;
XX
XX DT 02-OCT-1996 (first entry)
XX
XX DE Hepatitis C virus isolate T9 core protein.
XX
XX HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
XX hepatitis.
XX
XX OS Hepatitis C virus.
XX
XX PN WO9605315-A2.
XX
XX PD 22-FEB-1996.
XX
XX PF 15-AUG-1995; 95WO-US010398.
XX
XX PR 15-AUG-1994; 94US-00290665.
XX
XX PA (USSH ) US SEC DEPT HEALTH.
XX
XX PI Bukh J, Miller RH, Purcell RH;
XX
XX WPI; 1996-139709/14.
XX N-FSDB; AAT16635.
XX
XX DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
XX determine HCV genotype and as vaccines against HCV infection.
XX
XX PS Claim 4; Page 201-202; 340pp; English.
XX
XX CC AAR92936-R92987 are HCV core proteins derived from 52 different HCV
XX isolates. Isolated cDNA sequences are used for the prodn. of primers
XX useful for detecting the presence of HCV in a sample, the primers are
XX also useful for HCV genotyping. Proteins encoded by the cDNAs can be used
XX in vaccines for immunising against HCV infection. The proteins may also
XX be used to detect antibodies against HCV in serum, saliva, lymphocytes or
XX other mononuclear cells. The antibodies may be used in the prevention of
XX HCV infection
XX
XX SQ Sequence 191 AA;
XX
XX Query Match 91.5%; Score 43; DB 2; Length 191;
XX Best Local Similarity 88.9%; Pred. No. 1.8;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 DLMGYIPAV 9
XX |||||
XX Db 132 DLMGYIPV 140
XX
XX RESULT 27
XX AAR92961
XX ID AAR92961 standard; protein; 191 AA.
XX
XX AC AAR92961;
XX
XX DT 02-OCT-1996 (first entry)
XX
XX DE Hepatitis C virus isolate T2 core protein.
XX
XX HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
XX hepatitis.
XX
XX OS Hepatitis C virus.
XX
XX PN WO9605315-A2.
XX
XX PD 22-FEB-1996.
XX
XX PF 15-AUG-1995; 95WO-US010398.
XX
XX PR 15-AUG-1994; 94US-00290665.
XX
XX PA (USSH ) US SEC DEPT HEALTH.
XX
XX PI Bukh J, Miller RH, Purcell RH;
XX
XX WPI; 1996-139709/14.
XX N-FSDB; AAT16635.
XX
XX DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
XX determine HCV genotype and as vaccines against HCV infection.
XX
XX PS Claim 4; Page 201-202; 340pp; English.
XX
XX CC AAR92936-R92987 are HCV core proteins derived from 52 different HCV
XX isolates. Isolated cDNA sequences are used for the prodn. of primers
XX useful for detecting the presence of HCV in a sample, the primers are
XX also useful for HCV genotyping. Proteins encoded by the cDNAs can be used

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CC in vaccines for immunising against HCV infection. The proteins may also
 CC be used to detect antibodies against HCV in serum, saliva, lymphocytes or
 CC other mononuclear cells. The antibodies may be used in the prevention of
 CC HCV infection

XX SQ Sequence 191 AA;

Query Match 91.5%; Score 43; DB 2; Length 191;
 Best Local Similarity 88.9%; Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 |||||
 Db 132 DLMGYIPV 140

RESULT 28

AAR92978
 ID AAR92978 standard; protein; 191 AA.

XX AC AAR92978;

XX DT 02-OCT-1996 (first entry)

XX DE Hepatitis C virus isolate DK13 core protein.

XX KW HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
 XX hepatitis.

XX OS Hepatitis C virus.

XX PN WO9605315-A2.

XX PD 22-FEB-1996.

XX PF 15-AUG-1995; 95WO-US010398.

XX PR 15-AUG-1994; 94US-00290665.

XX PA (USSH) US SEC DEPT HEALTH.

XX PI Bukh J, Miller RH, Purcell RH;

XX DR WPI; 1996-139709/14.

XX DR N-PSDB; AAT16652.

XX PT DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
 XX determine HCV genotype and as vaccines against HCV infection.

XX PS Claim 4; Page 215-216; 340pp; English.

XX CC AAR92936-R92987 are HCV core proteins derived from 52 different HCV
 CC isolates. Isolated cDNA sequences are used for the prodn. of primers
 CC useful for detecting the presence of HCV in a sample, the primers are
 CC also useful for HCV genotyping. Proteins encoded by the cDNAs can be used
 CC in vaccines for immunising against HCV infection. The proteins may also
 CC be used to detect antibodies against HCV in serum, saliva, lymphocytes or
 CC other mononuclear cells. The antibodies may be used in the prevention of
 CC HCV infection

XX SQ Sequence 191 AA;

Query Match 91.5%; Score 43; DB 2; Length 191;
 Best Local Similarity 88.9%; Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 |||||
 Db 132 DLMGYIPV 140

RESULT 29

AAR92966

ID AAR92966 standard; protein; 191 AA.

XX AC AAR92966;

XX DT 02-OCT-1996 (first entry)

XX DE Hepatitis C virus isolate DK8 core protein.

XX KW HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
 XX hepatitis.

XX OS Hepatitis C virus.

XX PN WO9605315-A2.

XX PD 22-FEB-1996.

XX PF 15-AUG-1995; 95WO-US010398.

XX PR 15-AUG-1994; 94US-00290665.

XX PA (USSH) US SEC DEPT HEALTH.

XX PI Bukh J, Miller RH, Purcell RH;

XX DR WPI; 1996-139709/14.

XX DR N-PSDB; AAT16640.

XX PT DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
 XX determine HCV genotype and as vaccines against HCV infection.

XX PS Claim 4; Page 205-206; 340pp; English.

XX CC AAR92936-R92987 are HCV core proteins derived from 52 different HCV
 CC isolates. Isolated cDNA sequences are used for the prodn. of primers
 CC useful for detecting the presence of HCV in a sample, the primers are
 CC also useful for HCV genotyping. Proteins encoded by the cDNAs can be used
 CC in vaccines for immunising against HCV infection. The proteins may also
 CC be used to detect antibodies against HCV in serum, saliva, lymphocytes or
 CC other mononuclear cells. The antibodies may be used in the prevention of
 CC HCV infection

XX SQ Sequence 191 AA;

Query Match 91.5%; Score 43; DB 2; Length 191;
 Best Local Similarity 88.9%; Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 |||||
 Db 132 DLMGYIPV 140

RESULT 30

AAR92987

ID AAR92987 standard; protein; 191 AA.

XX AC AAR92987;

XX DT 02-OCT-1996 (first entry)

XX DE Hepatitis C virus isolate HK2 core protein.

XX KW HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
 XX hepatitis.

XX OS Hepatitis C virus.

XX PN WO9605315-A2.

XX PD 22-FEB-1996.

XX PF 15-AUG-1995; 95WO-US010398.

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XX PR 15-AUG-1994; 94US-00290665.
XX PA (USSH ) US SEC DEPT HEALTH.
XX PI Bukh J, Miller RH, Purcell RH;
XX PS WPI; 1996-139709/14.
XX DR N-PSDB; AAT16661.
XX PT DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
XX PT determine HCV genotype and as vaccines against HCV infection.
XX PS Claim 4; Page 223; 340pp; English.
XX CC AAR92936-R92987 are HCV core proteins derived from 52 different HCV
XX CC isolates. Isolated cDNA sequences are used for the prodn. of primers
XX CC useful for detecting the presence of HCV in a sample, the primers are
XX CC also useful for HCV genotyping. Proteins encoded by the cDNAs can be used
XX CC in vaccines for immunising against HCV infection. The proteins may also
XX CC be used to detect antibodies against HCV in serum, saliva, lymphocytes or
XX CC other mononuclear cells. The antibodies may be used in the prevention of
XX CC HCV infection
XX SQ Sequence 191 AA;
XX Query Match 91.5%; Score 43; DB 2; Length 191;
XX Best Local Similarity 88.9%; Pred. NO. 1.8;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
DB 132 DLMGYIPV 140

RESULT 31
AAR92959
ID AAR92959 standard; protein; 191 AA.
XX AC AAR92959;
XX DT 02-OCT-1996 (first entry)
XX DE Hepatitis C virus isolate US10 core protein.
XX HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
XX KW hepatitis.
XX OS Hepatitis C virus.
XX PN WO9605315-A2.
XX PD 22-FEB-1996.
XX PF 15-AUG-1995; 95WO-US010398.
XX PR 15-AUG-1994; 94US-00290665.
XX PA (USSH ) US SEC DEPT HEALTH.
XX PI Bukh J, Miller RH, Purcell RH;
XX WPI; 1996-139709/14.
XX DR N-PSDB; AAT16637.
XX PT DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
XX PT determine HCV genotype and as vaccines against HCV infection.
XX PS Claim 4; Page 199-200; 340pp; English.
XX CC AAR92936-R92987 are HCV core proteins derived from 52 different HCV
XX CC isolates. Isolated cDNA sequences are used for the prodn. of primers
XX CC useful for detecting the presence of HCV in a sample, the primers are
XX CC also useful for HCV genotyping. Proteins encoded by the cDNAs can be used
XX CC in vaccines for immunising against HCV infection. The proteins may also
XX CC be used to detect antibodies against HCV in serum, saliva, lymphocytes or
XX CC other mononuclear cells. The antibodies may be used in the prevention of
XX CC HCV infection
XX SQ Sequence 191 AA;
XX Query Match 91.5%; Score 43; DB 2; Length 191;
XX Best Local Similarity 88.9%; Pred. NO. 1.8;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
DB 132 DLMGYIPV 140

RESULT 32
AAR92963
ID AAR92963 standard; protein; 191 AA.
XX AC AAR92963;
XX DT 02-OCT-1996 (first entry)
XX DE Hepatitis C virus isolate US1 core protein.
XX HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
XX KW hepatitis.
XX OS Hepatitis C virus.
XX PN WO9605315-A2.
XX PD 22-FEB-1996.
XX PF 15-AUG-1995; 95WO-US010398.
XX PR 15-AUG-1994; 94US-00290665.
XX PA (USSH ) US SEC DEPT HEALTH.
XX PI Bukh J, Miller RH, Purcell RH;
XX WPI; 1996-139709/14.
XX DR N-PSDB; AAT16637.
XX PT DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
XX PT determine HCV genotype and as vaccines against HCV infection.
XX PS Claim 4; Page 203; 340pp; English.
XX CC AAR92936-R92987 are HCV core proteins derived from 52 different HCV
XX CC isolates. Isolated cDNA sequences are used for the prodn. of primers
XX CC useful for detecting the presence of HCV in a sample, the primers are
XX CC also useful for HCV genotyping. Proteins encoded by the cDNAs can be used
XX CC in vaccines for immunising against HCV infection. The proteins may also
XX CC be used to detect antibodies against HCV in serum, saliva, lymphocytes or
XX CC other mononuclear cells. The antibodies may be used in the prevention of
XX CC HCV infection
XX SQ Sequence 191 AA;
XX Query Match 91.5%; Score 43; DB 2; Length 191;
XX Best Local Similarity 88.9%; Pred. NO. 1.8;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
DB 132 DLMGYIPV 140

RESULT 33

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CC also useful for HCV genotyping. Proteins encoded by the cDNAs can be used
CC in vaccines for immunising against HCV infection. The proteins may also
CC be used to detect antibodies against HCV in serum, saliva, lymphocytes or
CC other mononuclear cells. The antibodies may be used in the prevention of
CC HCV infection
XX SQ Sequence 191 AA;
XX Query Match 91.5%; Score 43; DB 2; Length 191;
XX Best Local Similarity 88.9%; Pred. NO. 1.8;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
DB 132 DLMGYIPV 140

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RESULT 32
AAR92963
ID AAR92963 standard; protein; 191 AA.
XX AC AAR92963;
XX DT 02-OCT-1996 (first entry)
XX DE Hepatitis C virus isolate US1 core protein.
XX HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
XX KW hepatitis.
XX OS Hepatitis C virus.
XX PN WO9605315-A2.
XX PD 22-FEB-1996.
XX PF 15-AUG-1995; 95WO-US010398.
XX PR 15-AUG-1994; 94US-00290665.
XX PA (USSH ) US SEC DEPT HEALTH.
XX PI Bukh J, Miller RH, Purcell RH;
XX WPI; 1996-139709/14.
XX DR N-PSDB; AAT16637.
XX PT DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
XX PT determine HCV genotype and as vaccines against HCV infection.
XX PS Claim 4; Page 203; 340pp; English.
XX CC AAR92936-R92987 are HCV core proteins derived from 52 different HCV
XX CC isolates. Isolated cDNA sequences are used for the prodn. of primers
XX CC useful for detecting the presence of HCV in a sample, the primers are
XX CC also useful for HCV genotyping. Proteins encoded by the cDNAs can be used
XX CC in vaccines for immunising against HCV infection. The proteins may also
XX CC be used to detect antibodies against HCV in serum, saliva, lymphocytes or
XX CC other mononuclear cells. The antibodies may be used in the prevention of
XX CC HCV infection
XX SQ Sequence 191 AA;
XX Query Match 91.5%; Score 43; DB 2; Length 191;
XX Best Local Similarity 88.9%; Pred. NO. 1.8;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
DB 132 DLMGYIPV 140

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RESULT 33

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AAR92964
ID AAR92964 standard; protein; 191 AA.
XX
AC AAR92964;
XX
DT 02-OCT-1996 (first entry)
XX
DE Hepatitis C virus isolate DX11 core protein.
XX
KW HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
KW hepatitis.
XX
OS Hepatitis C virus.
XX
PN WO9605315-A2.
XX
PD 22-FEB-1996.
XX
PF 15-AUG-1995; 95WO-US010398.
XX
PR 15-AUG-1994; 94US-00290665.
XX
PA (USSH ) US SEC DEPT HEALTH.
XX
PI Bukh J, Miller RH, Purcell RH;
XX
DR WPI; 1996-139709/14.
DR N-PSDB; AAT16638.
XX
PT DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
PT determine HCV genotype and as vaccines against HCV infection.
XX
PS Claim 4; Page 204; 340pp; English.
XX
CC AAR92936-R92987 are HCV core proteins derived from 52 different HCV
CC isolates. Isolated cDNA sequences are used for the prodn. of primers
CC useful for detecting the presence of HCV in a sample, the primers are
CC also useful for HCV genotyping. Proteins encoded by the cDNAs can be used
CC in vaccines for immunising against HCV infection. The proteins may also
CC be used to detect antibodies against HCV infection. The proteins may also
CC other mononuclear cells. The antibodies may be used in the prevention of
CC HCV infection
XX
SQ Sequence 191 AA;
XX
Query Match 91.5%; Score 43; DB 2; Length 191;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLGMYIPAV 9
DB 132 DLGMYIPV 140
|||||
RESULT 34
AAR92965
ID AAR92965 standard; protein; 191 AA.
XX
AC AAR92965;
XX
DT 02-OCT-1996 (first entry)
XX
DE Hepatitis C virus isolate SW3 core protein.
XX
KW HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
KW hepatitis.
XX
OS Hepatitis C virus.
XX
PN WO9605315-A2.
XX
PD 22-FEB-1996.
XX
PF 15-AUG-1995; 95WO-US010398.
XX
PR 15-AUG-1994; 94US-00290665.
XX
PA (USSH ) US SEC DEPT HEALTH.
XX
PI Bukh J, Miller RH, Purcell RH;
XX
DR WPI; 1996-139709/14.
DR N-PSDB; AAT16641.
XX
PT DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
PT determine HCV genotype and as vaccines against HCV infection.
XX
PS Claim 4; Page 206-207; 340pp; English.
XX
CC AAR92936-R92987 are HCV core proteins derived from 52 different HCV
CC isolates. Isolated cDNA sequences are used for the prodn. of primers

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PF 15-AUG-1995; 95WO-US010398.
XX
PR 15-AUG-1994; 94US-00290665.
XX
PA (USSH ) US SEC DEPT HEALTH.
XX
PI Bukh J, Miller RH, Purcell RH;
XX
DR WPI; 1996-139709/14.
DR N-PSDB; AAT16639.
XX
PT DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
PT determine HCV genotype and as vaccines against HCV infection.
XX
PS Claim 4; Page 204-205; 340pp; English.
XX
CC AAR92936-R92987 are HCV core proteins derived from 52 different HCV
CC isolates. Isolated cDNA sequences are used for the prodn. of primers
CC useful for detecting the presence of HCV in a sample, the primers are
CC also useful for HCV genotyping. Proteins encoded by the cDNAs can be used
CC in vaccines for immunising against HCV infection. The proteins may also
CC be used to detect antibodies against HCV infection. The proteins may also
CC other mononuclear cells. The antibodies may be used in the prevention of
CC HCV infection
XX
SQ Sequence 191 AA;
XX
Query Match 91.5%; Score 43; DB 2; Length 191;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLGMYIPAV 9
DB 132 DLGMYIPV 140
|||||
RESULT 35
AAR92967
ID AAR92967 standard; protein; 191 AA.
XX
AC AAR92967;
XX
DT 02-OCT-1996 (first entry)
XX
DE Hepatitis C virus isolate S83 core protein.
XX
KW HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
KW hepatitis.
XX
OS Hepatitis C virus.
XX
PN WO9605315-A2.
XX
PD 22-FEB-1996.
XX
PF 15-AUG-1995; 95WO-US010398.
XX
PR 15-AUG-1994; 94US-00290665.
XX
PA (USSH ) US SEC DEPT HEALTH.
XX
PI Bukh J, Miller RH, Purcell RH;
XX
DR WPI; 1996-139709/14.
DR N-PSDB; AAT16641.
XX
PT DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
PT determine HCV genotype and as vaccines against HCV infection.
XX
PS Claim 4; Page 206-207; 340pp; English.
XX
CC AAR92936-R92987 are HCV core proteins derived from 52 different HCV
CC isolates. Isolated cDNA sequences are used for the prodn. of primers

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CC useful for detecting the presence of HCV in a sample, the primers are
 CC also useful for HCV genotyping. Proteins encoded by the cDNAs can be used
 CC in vaccines for immunising against HCV infection. The proteins may also
 CC be used to detect antibodies against HCV in serum, saliva, lymphocytes or
 CC other mononuclear cells. The antibodies may be used in the prevention of
 CC HCV infection

XX Sequence 191 AA;

SQ Query Match 91.5%; Score 43; DB 2; Length 191;
 Best Local Similarity 88.9%; Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 |||||
 DB 132 DLMGYIPV 140

RESULT 36

AAR92962
 ID AAR92962 standard; protein; 191 AA.

XX AC AAR92962;

DT 02-OCT-1996 (first entry)

XX Hepatitis C virus isolate T8 core protein.

DE HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
 KW hepatitis.

XX Hepatitis C virus.

OS WO9605315-A2.

PN 22-FEB-1996.

XX 15-AUG-1995; 95WO-US010398.

PR 15-AUG-1994; 94US-00290665.

XX (USSH) US SEC DEPT HEALTH.

PI Bukh J, Miller RH, Purcell RH;

XX WPI; 1996-139709/14.

DR N-PSDB; AAT16636.

XX DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
 PT determine HCV genotype and as vaccines against HCV infection.

PS Claim 4; Page 202; 340pp; English.

XX AAR92936-R32987 are HCV core proteins derived from 52 different HCV
 CC isolates. Isolated cDNA sequences are used for the prodn. of primers
 CC useful for detecting the presence of HCV in a sample, the primers are
 CC also useful for HCV genotyping. Proteins encoded by the cDNAs can be used
 CC in vaccines for immunising against HCV infection. The proteins may also
 CC be used to detect antibodies against HCV in serum, saliva, lymphocytes or
 CC other mononuclear cells. The antibodies may be used in the prevention of
 CC HCV infection

XX Sequence 191 AA;

SQ Query Match 91.5%; Score 43; DB 2; Length 191;
 Best Local Similarity 88.9%; Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 |||||
 DB 132 DLMGYIPV 140

RESULT 37
 AAW41755
 ID AAW41755 standard; protein; 193 AA.

XX AC AAW41755;

DT 22-MAY-1998 (first entry)

XX Hepatitis C virus antigen.

DE non-A non-B hepatitis virus; NANBH; hepatitis C virus; HCV; antigen;
 KW diagnosis; detection.

OS Hepatitis virus.

XX JP05176774-A.

PN 20-JUL-1993.

XX 18-DEC-1991; 91JP-00354708.

PR 18-DEC-1990; 90JP-00412020.

XX (SHIM/) SHIMOTONO K.

PA (GREC) GREEN CROSS CORP.

XX WPI; 1993-260858/33.

DR Protein contg. non-A non-B hepatitis antigen fragment - prepd. by
 PT culturing transformants transformed by vector contg. base sequence coding
 PT specified aminoacid sequences, used for detecting hepatitis.

XX Claim 1; Fig 61; 53pp; Japanese.

CC The present sequence is a non-A non-B hepatitis virus (NANBH) or
 CC hepatitis C virus (HCV) antigen, useful for diagnosis or detection

SQ Sequence 193 AA;

Query Match 91.5%; Score 43; DB 2; Length 193;
 Best Local Similarity 88.9%; Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9

DB 137 DLMGYIPV 145

RESULT 38
 ABP55560
 ID ABP55560 standard; protein; 209 AA.

XX AC ABP55560;

DT 19-FEB-2003 (first entry)

DE Hepatitis C virus protein SEQ ID NO:90.

XX Hepatitis C virus; HCV; envelope protein; hepatotropic; virucide;
 KW antiinflammatory; gene therapy; vaccine.

OS Hepatitis C virus.

XX WO200285932-A2.

PN 31-OCT-2002.

XX 24-APR-2002; 2002WO-BE000062.

XX 24-APR-2001; 2001EP-00870088.

PR 17-JUL-2001; 2001US-0305604P.

XX (INNO-) INNOGENETICS NV.

XX Sablon E, Van Broekhoven A, Bosman A, Depla E, Deschamps G;
 PI WPI; 2003-093095/08.
 XX
 XX New recombinant nucleic acids for expressing Hepatitis C virus (HCV)
 PT envelope proteins in eukaryotic cells, comprising a sequence encoding a
 PT protein having an avian lysozyme leader peptide joined to the HCV
 PT envelope protein.
 XX
 XX Claim 5; Page 309-310; 319pp; English.
 XX
 CC The present invention describes a recombinant nucleic acid (I) comprising
 CC a nucleotide sequence encoding a protein having an avian lysozyme leader
 CC peptide, or its functional equivalent, joined to a Hepatitis C virus
 CC (HCV) envelope protein or its part. Also described: (1) a vector
 CC comprising the recombinant nucleic acid; (2) a host cell comprising the
 CC recombinant nucleic acid or the vector; and (3) a method for producing
 CC HCV envelope protein or its part in a host cell, comprising transforming
 CC the host cell with the recombinant nucleic acid or with the vector, where
 CC the host cell is capable of expressing the protein cited above. (I) has
 CC hepatotropic, virucide and antiinflammatory activities, and can be used
 CC in gene therapy and vaccines. The recombinant nucleic acid is useful for
 CC efficient expression of Hepatitis C virus envelope proteins in eukaryotic
 CC cells, such as yeast cells. The HCV envelope proteins may be used as a
 CC vaccine, or for incorporation into an immunoassay for the detection of
 CC anti-HCV antibodies, and/or genotyping of HCV, for prognosing or
 CC monitoring of HCV disease, or as a therapeutic agent. The method is used
 CC for producing HCV envelope protein or its part in a host cell. ABQ84197
 CC to ABQ84253 and ABP55528 to ABP55568 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 209 AA;
 Query Match 91.5%; Score 43; DB 6; Length 209;
 Best Local Similarity 88.9%; Pred. No. 2;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 DLMGYIPAV 9
 Db 15 DLMGYIPV 23
 RESULT 39
 ABP55559
 ID ABP55559 standard; protein; 209 AA.
 XX
 XX AC ABP55559;
 XX
 DT 19-FEB-2003 (first entry)
 XX
 DE Hepatitis C virus protein SEQ ID NO:89.
 XX
 KW Hepatitis C virus; HCV; envelope protein; hepatotropic; virucide;
 KW antiinflammatory; gene therapy; vaccine.
 XX
 OS Hepatitis C virus.
 XX
 XX WO200285932-A2.
 XX
 XX 31-OCT-2002.
 XX
 XX 24-APR-2002; 2002WO-BE000062.
 XX
 XX 24-APR-2001; 2001EP-00870088.
 PR 17-JUL-2001; 2001US-0305604P.
 XX
 XX (INNO-) INNOGENETICS NV.
 XX
 XX Sablon E, Van Broekhoven A, Bosman A, Depla E, Deschamps G;
 PI WPI; 2003-093095/08.
 XX
 XX New recombinant nucleic acids for expressing Hepatitis C virus (HCV)
 PT envelope proteins in eukaryotic cells, comprising a sequence encoding a
 PT protein having an avian lysozyme leader peptide joined to the HCV
 PT envelope protein.
 XX
 XX Claim 5; Page 308-309; 319pp; English.
 XX
 CC The present invention describes a recombinant nucleic acid (I) comprising
 CC a nucleotide sequence encoding a protein having an avian lysozyme leader
 CC peptide, or its functional equivalent, joined to a Hepatitis C virus
 CC (HCV) envelope protein or its part. Also described: (1) a vector
 CC comprising the recombinant nucleic acid; (2) a host cell comprising the
 CC recombinant nucleic acid or the vector; and (3) a method for producing
 CC HCV envelope protein or its part in a host cell, comprising transforming
 CC the host cell with the recombinant nucleic acid or with the vector, where
 CC the host cell is capable of expressing the protein cited above. (I) has
 CC hepatotropic, virucide and antiinflammatory activities, and can be used
 CC in gene therapy and vaccines. The recombinant nucleic acid is useful for
 CC efficient expression of Hepatitis C virus envelope proteins in eukaryotic
 CC cells, such as yeast cells. The HCV envelope proteins may be used as a
 CC vaccine, or for incorporation into an immunoassay for the detection of
 CC anti-HCV antibodies, and/or genotyping of HCV, for prognosing or
 CC monitoring of HCV disease, or as a therapeutic agent. The method is used
 CC for producing HCV envelope protein or its part in a host cell. ABQ84197
 CC to ABQ84253 and ABP55528 to ABP55568 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 209 AA;
 Query Match 91.5%; Score 43; DB 6; Length 209;
 Best Local Similarity 88.9%; Pred. No. 2;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 DLMGYIPAV 9
 Db 15 DLMGYIPV 23
 RESULT 40
 ABP55564
 ID ABP55564 standard; protein; 209 AA.
 XX
 XX AC ABP55564;
 XX
 DT 19-FEB-2003 (first entry)
 XX
 DE Hepatitis C virus protein SEQ ID NO:94.
 XX
 KW Hepatitis C virus; HCV; envelope protein; hepatotropic; virucide;
 KW antiinflammatory; gene therapy; vaccine.
 XX
 OS Hepatitis C virus.
 XX
 XX WO200285932-A2.
 XX
 XX 31-OCT-2002.
 XX
 XX 24-APR-2002; 2002WO-BE000062.
 XX
 XX 24-APR-2001; 2001EP-00870088.
 PR 17-JUL-2001; 2001US-0305604P.
 XX
 XX (INNO-) INNOGENETICS NV.
 XX
 XX Sablon E, Van Broekhoven A, Bosman A, Depla E, Deschamps G;
 PI WPI; 2003-093095/08.
 XX
 XX New recombinant nucleic acids for expressing Hepatitis C virus (HCV)
 PT envelope proteins in eukaryotic cells, comprising a sequence encoding a
 PT protein having an avian lysozyme leader peptide joined to the HCV
 PT envelope protein.
 XX

PT New recombinant nucleic acids for expressing Hepatitis C virus (HCV)
 PT envelope proteins in eukaryotic cells, comprising a sequence encoding a
 PT protein having an avian lysozyme leader peptide joined to the HCV
 PT envelope protein.
 XX
 XX Claim 5; Page 308-309; 319pp; English.
 XX
 CC The present invention describes a recombinant nucleic acid (I) comprising
 CC a nucleotide sequence encoding a protein having an avian lysozyme leader
 CC peptide, or its functional equivalent, joined to a Hepatitis C virus
 CC (HCV) envelope protein or its part. Also described: (1) a vector
 CC comprising the recombinant nucleic acid; (2) a host cell comprising the
 CC recombinant nucleic acid or the vector; and (3) a method for producing
 CC HCV envelope protein or its part in a host cell, comprising transforming
 CC the host cell with the recombinant nucleic acid or with the vector, where
 CC the host cell is capable of expressing the protein cited above. (I) has
 CC hepatotropic, virucide and antiinflammatory activities, and can be used
 CC in gene therapy and vaccines. The recombinant nucleic acid is useful for
 CC efficient expression of Hepatitis C virus envelope proteins in eukaryotic
 CC cells, such as yeast cells. The HCV envelope proteins may be used as a
 CC vaccine, or for incorporation into an immunoassay for the detection of
 CC anti-HCV antibodies, and/or genotyping of HCV, for prognosing or
 CC monitoring of HCV disease, or as a therapeutic agent. The method is used
 CC for producing HCV envelope protein or its part in a host cell. ABQ84197
 CC to ABQ84253 and ABP55528 to ABP55568 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 209 AA;
 Query Match 91.5%; Score 43; DB 6; Length 209;
 Best Local Similarity 88.9%; Pred. No. 2;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 DLMGYIPAV 9
 Db 15 DLMGYIPV 23
 RESULT 40
 ABP55564
 ID ABP55564 standard; protein; 209 AA.
 XX
 XX AC ABP55564;
 XX
 DT 19-FEB-2003 (first entry)
 XX
 DE Hepatitis C virus protein SEQ ID NO:94.
 XX
 KW Hepatitis C virus; HCV; envelope protein; hepatotropic; virucide;
 KW antiinflammatory; gene therapy; vaccine.
 XX
 OS Hepatitis C virus.
 XX
 XX WO200285932-A2.
 XX
 XX 31-OCT-2002.
 XX
 XX 24-APR-2002; 2002WO-BE000062.
 XX
 XX 24-APR-2001; 2001EP-00870088.
 PR 17-JUL-2001; 2001US-0305604P.
 XX
 XX (INNO-) INNOGENETICS NV.
 XX
 XX Sablon E, Van Broekhoven A, Bosman A, Depla E, Deschamps G;
 PI WPI; 2003-093095/08.
 XX
 XX New recombinant nucleic acids for expressing Hepatitis C virus (HCV)
 PT envelope proteins in eukaryotic cells, comprising a sequence encoding a
 PT protein having an avian lysozyme leader peptide joined to the HCV
 PT envelope protein.
 XX

PS Claim 5; Page 313-314; 319pp; English.

XX
CC The present invention describes a recombinant nucleic acid (1) comprising
CC a nucleotide sequence encoding a protein having an avian lysozyme leader
CC peptide, or its functional equivalent, joined to a Hepatitis C virus
CC (HCV) envelope protein or its part. Also described: (1) a vector
CC comprising the recombinant nucleic acid; (2) a host cell comprising the
CC recombinant nucleic acid or the vector; and (3) a method for producing
CC HCV envelope protein or its part in a host cell, comprising transforming
CC the host cell with the recombinant nucleic acid or with the vector, where
CC the host cell is capable of expressing the protein cited above. (1) has
CC hepatotropic, virucide and antiinflammatory activities, and can be used
CC in gene therapy and vaccines. The recombinant nucleic acid is useful for
CC efficient expression of Hepatitis C virus envelope proteins in eukaryotic
CC cells, such as yeast cells. The HCV envelope proteins may be used as a
CC vaccine, or for incorporation into an immunoassay for the detection of
CC anti-HCV antibodies, and/or genotyping of HCV, for prognosing or
CC monitoring of HCV disease, or as a therapeutic agent. The method is used
CC for producing HCV envelope protein or its part in a host cell. AB084197
CC to ABQ84253 and ABP55528 to ABP55568 represent sequences used in the
CC exemplification of the present invention

XX
SQ Sequence 209 AA;

Query Match 91.5%; Score 43; DB 6; Length 209;
Best Local Similarity 88.9%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 15 DLMGYIPV 23
|||||

Search completed: January 20, 2006, 22:40:13
Job time : 81 secs

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OM protein - protein search, using sw model

Run on: January 20, 2006, 22:38:08 ; Search time 23 Seconds

(without alignments)

32.351 Million cell updates/sec

Title: US-10-770-117-1

Perfect score: 47

Sequence: 1 DLMGYIPAV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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14	43	91.5	191	4	PCT-US95-10398-178
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21	43	91.5	191	4	PCT-US95-10398-185
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26	43	91.5	193	2	US-08-974-690C-203
27	43	91.5	304	2	US-08-635-886C-204

28	43	91.5	304	2	US-08-974-690C-204
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30	43	91.5	319	2	US-08-836-075A-18
31	43	91.5	319	2	US-08-836-075A-44
32	43	91.5	319	2	US-08-635-886C-202
33	43	91.5	319	2	US-08-635-886C-206
34	43	91.5	319	2	US-08-635-886C-217
35	43	91.5	319	2	US-08-635-886C-228
36	43	91.5	319	2	US-08-635-886C-230
37	43	91.5	319	2	US-08-974-690C-202
38	43	91.5	319	2	US-08-974-690C-206
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52	42	89.4	9	2	US-08-197-484-51
53	42	89.4	9	2	US-08-197-484-130
54	42	89.4	9	2	US-09-311-784A-255
55	42	89.4	9	2	US-09-763-260-3
56	42	89.4	9	4	PCT-US95-02121-51
57	42	89.4	9	4	PCT-US95-02121-130
58	42	89.4	10	1	US-08-214-650-1
59	42	89.4	15	2	US-09-009-953-172
60	42	89.4	16	1	US-08-986-234-34
61	42	89.4	20	2	US-08-635-886C-10
62	42	89.4	20	2	US-08-974-690C-10
63	42	89.4	20	2	US-08-974-685-10
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66	42	89.4	25	2	US-10-173-480-58
67	42	89.4	25	2	US-10-173-480-59
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70	42	89.4	37	2	US-08-635-886C-281
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79	42	89.4	150	1	US-08-485-500-16
80	42	89.4	150	4	PCT-US91-02370-16
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84	42	89.4	166	2	US-09-878-281A-152
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86	42	89.4	166	2	US-09-878-281A-194
87	42	89.4	169	2	US-08-444-818-93
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90	42	89.4	181	2	US-08-635-886C-182
91	42	89.4	181	2	US-08-974-690C-182
92	42	89.4	182	2	US-10-104-966-2
93	42	89.4	182	2	US-09-929-955-2
94	42	89.4	190	1	US-07-681-701-16
95	42	89.4	190	2	US-08-078-271B-1
96	42	89.4	191	1	US-08-290-665A-155
97	42	89.4	191	1	US-08-290-665A-156
98	42	89.4	191	1	US-08-290-665A-157
99	42	89.4	191	1	US-08-290-665A-158
100	42	89.4	191	1	US-08-290-665A-159

ALIGNMENTS

RESULT 1
US-09-763-260-1
; Sequence 1, Application US/09763260
; Patent No. 6685944
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States, as represented by the
; APPLICANT: Secretary, Dept. of
; APPLICANT: Health and Human Services
; APPLICANT: Berzofsky, Jay A.
; APPLICANT: Sarobe, Pablo
; APPLICANT: Pendleton, C. David
; APPLICANT: Feinstein, Stephen M.
; APPLICANT: Arichi, Tatsumi
; APPLICANT: Major, Marian E.
; FILE OF INVENTION: MODIFIED HCV PEPTIDE VACCINES
; FILE REFERENCE: 14014.0347/P
; CURRENT APPLICATION NUMBER: US/09/763,260
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/097,446
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. 6685944e =
; OTHER INFORMATION: synthetic construct
US-09-763-260-1

Query Match 100.0%; Score 47; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
| | | | |
DB 1 DLMGYIPAV 9

RESULT 2
US-09-763-260-2
; Sequence 2, Application US/09763260
; Patent No. 6685944
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States, as represented by the
; APPLICANT: Secretary, Dept. of
; APPLICANT: Health and Human Services
; APPLICANT: Berzofsky, Jay A.
; APPLICANT: Sarobe, Pablo
; APPLICANT: Pendleton, C. David
; APPLICANT: Feinstein, Stephen M.
; APPLICANT: Arichi, Tatsumi
; APPLICANT: Major, Marian E.
; FILE OF INVENTION: MODIFIED HCV PEPTIDE VACCINES
; FILE REFERENCE: 14014.0347/P
; CURRENT APPLICATION NUMBER: US/09/763,260
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/097,446
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. 6685944e =

; OTHER INFORMATION: synthetic construct
US-09-763-260-2

Query Match 100.0%; Score 47; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
| | | | |
DB 132 DLMGYIPAV 140

RESULT 3
US-08-290-665A-178
; Sequence 178, Application US/08290665A
; Patent No. 5882852
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,665A
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: US10
US-08-290-665A-178

Query Match 91.5%; Score 43; DB 1; Length 191;
Best Local Similarity 88.9%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
| | | | |
DB 132 DLMGYIPAV 140

RESULT 4
US-08-290-665A-179
; Sequence 179, Application US/08290665A
; Patent No. 5882852

```

; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,665A
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 179:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; ORGANISM: homosaapiens
; INDIVIDUAL ISOLATE: T9
; ORIGINAL SOURCE:
; US-08-290-665A-179
;
; Query Match 91.5%; Score 43; DB 1; Length 191;
; Best Local Similarity 88.9%; Pred. No. 0.45;
; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1 DLMGYIPAV 9
; Db 132 DLMGYIPV 140
;
; RESULT 5
; US-08-290-665A-180
; Sequence 180, Application US/08290665A
; Patent No. 5882852
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,665A
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; ORGANISM: homosaapiens
; INDIVIDUAL ISOLATE: T2
; ORIGINAL SOURCE:
; US-08-290-665A-180
;
; Query Match 91.5%; Score 43; DB 1; Length 191;
; Best Local Similarity 88.9%; Pred. No. 0.45;
; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1 DLMGYIPAV 9
; Db 132 DLMGYIPV 140
;
; RESULT 6
; US-08-290-665A-181
; Sequence 181, Application US/08290665A
; Patent No. 5882852
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,665A
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792

```

TELEX: 421792
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: T8
US-08-290-665A-181

Query Match 91.5%; Score 43; DB 1; Length 191;
Best Local Similarity 88.9%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPV 9
Db 132 DLMGYIPV 140

RESULT 7
US-08-290-665A-182
; Sequence 182, Application US/08290665A
; Patent No. 5882852
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,665A
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 182:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: US1
US-08-290-665A-182

Query Match 91.5%; Score 43; DB 1; Length 191;
Best Local Similarity 88.9%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPV 9
Db 132 DLMGYIPV 140

RESULT 8
US-08-290-665A-183
; Sequence 183, Application US/08290665A
; Patent No. 5882852
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,665A
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: DK11
US-08-290-665A-183

Query Match 91.5%; Score 43; DB 1; Length 191;
Best Local Similarity 88.9%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPV 9
Db 132 DLMGYIPV 140

RESULT 9
US-08-290-665A-184
; Sequence 184, Application US/08290665A
; Patent No. 5882852
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE

```

; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,665A
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 184:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: SW3
; US-08-290-665A-184

Query Match 91.5%; Score 43; DB 1; Length 191;
Best Local Similarity 88.9%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
| | | | | | |
DB 132 DLMGYIPV 140

RESULT 10
; US-08-290-665A-185
; Sequence 185, Application US/08290665A
; Patent No. 5882852
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,665A
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; APPLICATION NUMBER: US/08/290,665A

```

```

; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 185:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: DK8
; US-08-290-665A-185

Query Match 91.5%; Score 43; DB 1; Length 191;
Best Local Similarity 88.9%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
| | | | | | |
DB 132 DLMGYIPV 140

RESULT 11
; US-08-290-665A-186
; Sequence 186, Application US/08290665A
; Patent No. 5882852
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,665A
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; APPLICATION NUMBER: US/08/290,665A

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; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: S93
US-08-290-665A-186

Query Match          91.5%; Score 43; DB 1; Length 191;
Best Local Similarity 88.9%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 12
US-08-290-665A-197
; Sequence 197, Application US/08290665A
; Patent No. 5882852
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,665A
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: HK2
US-08-290-665A-206

Query Match          91.5%; Score 43; DB 1; Length 191;
Best Local Similarity 88.9%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 14
PCT-US95-10398-178
; Sequence 178, Application PC/TUS9510398
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA

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TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 180:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: T2
PCT-US95-10398-180

Query Match 91.5%; Score 43; DB 4; Length 191;
Best Local Similarity 88.9%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
| | | | | | | |
Db 132 DLMGYIPV 140

RESULT 17

PCT-US95-10398-181
; Sequence 181, Application PC/TUS9510398
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10398
; FILING DATE: 15-AUG-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,428
; FILING DATE: 29 JUNE 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/290/665
; FILING DATE: 15 AUGUST 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: T8

PCT-US95-10398-181

Query Match 91.5%; Score 43; DB 4; Length 191;
Best Local Similarity 88.9%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
| | | | | | | |
Db 132 DLMGYIPV 140

RESULT 18

PCT-US95-10398-182
; Sequence 182, Application PC/TUS9510398
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10398
; FILING DATE: 15-AUG-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,428
; FILING DATE: 29 JUNE 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/290/665
; FILING DATE: 15 AUGUST 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 182:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: US1
; PCT-US95-10398-182

Query Match 91.5%; Score 43; DB 4; Length 191;
Best Local Similarity 88.9%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
| | | | | | | |
Db 132 DLMGYIPV 140

```

RESULT 19
PCT-US95-10398-183
; Sequence 183, Application PC/TUS9510398
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10398
; FILING DATE: 15-AUG-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,428
; FILING DATE: 29 JUNE 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/290/665
; FILING DATE: 15 AUGUST 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: DK11
PCT-US95-10398-183

Query Match 91.5%; Score 43; DB 4; Length 191;
Best Local Similarity 88.9%; Pred.No. 0.45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 20
PCT-US95-10398-184
; Sequence 184, Application PC/TUS9510398
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10398
; FILING DATE: 15-AUG-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,428
; FILING DATE: 29 JUNE 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/290/665
; FILING DATE: 15 AUGUST 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: DK11
PCT-US95-10398-183

Query Match 91.5%; Score 43; DB 4; Length 191;
Best Local Similarity 88.9%; Pred.No. 0.45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

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; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10398
; FILING DATE: 15-AUG-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,428
; FILING DATE: 29 JUNE 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/290/665
; FILING DATE: 15 AUGUST 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 184:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: SW3
PCT-US95-10398-184

Query Match 91.5%; Score 43; DB 4; Length 191;
Best Local Similarity 88.9%; Pred.No. 0.45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 21
PCT-US95-10398-185
; Sequence 185, Application PC/TUS9510398
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: DK8
PCT-US95-10398-185

Query Match 91.5%; Score 43; DB 4; Length 191;
Best Local Similarity 88.9%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 22
PCT-US95-10398-186
Sequence 186, Application PC/TUS9510398
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665

FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: S83
PCT-US95-10398-186

Query Match 91.5%; Score 43; DB 4; Length 191;
Best Local Similarity 88.9%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 23
PCT-US95-10398-197
Sequence 197, Application PC/TUS9510398
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 197:
SEQUENCE CHARACTERISTICS:

1 LENGTH: 191 amino acids
1 TYPE: amino acid
1 STRANDEDNESS: unknown
1 TOPOLOGY: unknown
1 ORIGINAL SOURCE:
1 ORGANISM: homosapiens
1 INDIVIDUAL ISOLATE: DK13
PCT-US95-10398-197

Query Match 91.5%; Score 43; DB 4; Length 191;
Best Local Similarity 88.9%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 24
PCT-US95-10398-206
Sequence 206, Application PC/TUS9510398
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PORCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSER: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: HK2
PCT-US95-10398-206

Query Match 91.5%; Score 43; DB 4; Length 191;
Best Local Similarity 88.9%; Pred. No. 0.45;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 25
US-08-635-886C-203
Sequence 203, Application US/08635886C
Patent No. 6555114
GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, Robert
APPLICANT: MAERTENS, Geert
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
FILE REFERENCE: 2752-18
CURRENT APPLICATION NUMBER: US/08/635,886C
PRIOR FILING DATE: 1996-04-25
PRIOR APPLICATION NUMBER: PCT/EP94/03555
PRIOR FILING DATE: 1994-10-28
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PatentIn version 3.1
SEQ ID NO 203
LENGTH: 193
TYPE: PRT
ORGANISM: hepatitis C virus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (5)..(5)
OTHER INFORMATION: Xaa is any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (18)..(18)
OTHER INFORMATION: Xaa is any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (37)..(37)
OTHER INFORMATION: Xaa is any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (58)..(58)
OTHER INFORMATION: Xaa is any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (66)..(66)
OTHER INFORMATION: Xaa is any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (95)..(95)
OTHER INFORMATION: Xaa is any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (119)..(119)
OTHER INFORMATION: Xaa is any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (173)..(173)
OTHER INFORMATION: Xaa is any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (193)..(193)
OTHER INFORMATION: Xaa is any amino acid
US-08-635-886C-203

Query Match 91.5%; Score 43; DB 2; Length 193;
Best Local Similarity 88.9%; Pred. No. 0.46;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DLMGYIPAV 9

Db |||||||
6 DLMGYIPV 14

```
RESULT 26
US-08-974-690C-203
; Sequence 203, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 203
; LENGTH: 193
; TYPE: PRT
; ORGANISM: hepatitis C virus
; NAME/KEY: MISC_FEATURE
; LOCATION: (18)..(18)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (37)..(37)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (58)..(58)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (66)..(66)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (95)..(95)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (119)..(119)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (173)..(173)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (193)..(193)
; OTHER INFORMATION: Xaa is any amino acid
US-08-974-690C-203
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Query Match 91.5%; Score 43; DB 2; Length 193;
Best Local Similarity 88.9%; Pred. No. 0.46;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db |||||||
6 DLMGYIPV 14

```
RESULT 27
US-08-635-886C-204
; Sequence 204, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 204
; LENGTH: 304
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-204
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Query Match 91.5%; Score 43; DB 2; Length 304;
Best Local Similarity 88.9%; Pred. No. 0.77;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db |||||||
132 DLMGYIPV 140

```
RESULT 28
US-08-974-690C-204
; Sequence 204, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 204
; LENGTH: 304
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-204
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Query Match 91.5%; Score 43; DB 2; Length 304;
Best Local Similarity 88.9%; Pred. No. 0.77;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db |||||||
132 DLMGYIPV 140

RESULT 29
US-08-836-075A-76
; Sequence 76, Application US/08836075A
; Patent No. 6180768

```
/
/ GENERAL INFORMATION:
/ APPLICANT: MAERTENS, GEERT
/ TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
/ TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
/ NUMBER OF SEQUENCES: 207
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ARNOLD, WHITE & DURKEE
/ STREET: P.O. BOX 4433
/ CITY: HOUSTON
/ STATE: TEXAS
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM: floppy disk
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Microsoft Word 6.0 / ASCII text output
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/836,075A
/ FILING DATE: 21 Apr 1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/EP95/04155
/ FILING DATE: 23 Oct 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 94870166.9
/ FILING DATE: 21 Oct 1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 95870076.7
/ FILING DATE: 28 Jun 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KAMMERER, PATRICIA A.
/ REGISTRATION NUMBER: 29,775
/ REFERENCE/DOCKET NUMBER: INNS:004
/ INFORMATION FOR SEQ ID NO: 76:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 318 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-836-075A-76

Query Match 91.5%; Score 43; DB 2; Length 318;
Best Local Similarity 88.9%; Pred. No. 0.81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
DB 132 DLMGYIPV 140

RESULT 30
US-08-836-075A-18
/ Sequence 18, Application US/08836075A
/ Patent No. 6180768
/ GENERAL INFORMATION:
/ APPLICANT: MAERTENS, GEERT
/ TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
/ TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
/ NUMBER OF SEQUENCES: 207
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ARNOLD, WHITE & DURKEE
/ STREET: P.O. BOX 4433
/ CITY: HOUSTON
/ STATE: TEXAS
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM: floppy disk
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Microsoft Word 6.0 / ASCII text output
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/836,075A
/ FILING DATE: 21 Apr 1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/EP95/04155
/ FILING DATE: 23 Oct 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 94870166.9
/ FILING DATE: 21 Oct 1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 95870076.7
/ FILING DATE: 28 Jun 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KAMMERER, PATRICIA A.
/ REGISTRATION NUMBER: 29,775
/ INFORMATION FOR SEQ ID NO: 76:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 318 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-836-075A-76
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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Microsoft Word 6.0 / ASCII text output
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/836,075A
/ FILING DATE: 21 Apr 1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/EP95/04155
/ FILING DATE: 23 Oct 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 94870166.9
/ FILING DATE: 21 Oct 1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 95870076.7
/ FILING DATE: 28 Jun 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KAMMERER, PATRICIA A.
/ REGISTRATION NUMBER: 29,775
/ REFERENCE/DOCKET NUMBER: INNS:004
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 319 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-836-075A-18

Query Match 91.5%; Score 43; DB 2; Length 319;
Best Local Similarity 88.9%; Pred. No. 0.81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
DB 132 DLMGYIPV 140

RESULT 31
US-08-836-075A-44
/ Sequence 44, Application US/08836075A
/ Patent No. 6180768
/ GENERAL INFORMATION:
/ APPLICANT: MAERTENS, GEERT
/ TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
/ TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
/ NUMBER OF SEQUENCES: 207
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ARNOLD, WHITE & DURKEE
/ STREET: P.O. BOX 4433
/ CITY: HOUSTON
/ STATE: TEXAS
/ COUNTRY: USA
/ ZIP: 77210-4433
/ COMPUTER READABLE FORM: floppy disk
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Microsoft Word 6.0 / ASCII text output
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/836,075A
/ FILING DATE: 21 Apr 1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/EP95/04155
/ FILING DATE: 23 Oct 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 94870166.9
/ FILING DATE: 21 Oct 1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 95870076.7
/ FILING DATE: 28 Jun 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KAMMERER, PATRICIA A.
/ REGISTRATION NUMBER: 29,775
```

REFERENCE/DOCKET NUMBER: INNS:004
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-075A-44

Query Match 91.5%; Score 43; DB 2; Length 319;
Best Local Similarity 88.9%; Pred. No. 0.81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
| | | | | | | |
DB 132 DLMGYIPV 140

RESULT 32

US-08-635-886C-202
Sequence 202, Application US/08635886C
Patent No. 6555114
GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, Robert
APPLICANT: MAERTENS, Geert
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
FILE REFERENCE: 2752-18
CURRENT APPLICATION NUMBER: US/08/635,886C
PRIOR FILING DATE: 1996-04-25
PRIOR APPLICATION NUMBER: PCT/EP94/03555
PRIOR FILING DATE: 1994-10-28
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patent in version 3.1
SEQ ID NO 202
TYPE: PRT
ORGANISM: hepatitis C virus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (319)..(319)
OTHER INFORMATION: Xaa is any amino acid
US-08-635-886C-202

Query Match 91.5%; Score 43; DB 2; Length 319;
Best Local Similarity 88.9%; Pred. No. 0.81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
| | | | | | | |
DB 132 DLMGYIPV 140

RESULT 33

US-08-635-886C-206
Sequence 206, Application US/08635886C
Patent No. 6555114
GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, Robert
APPLICANT: MAERTENS, Geert
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
FILE REFERENCE: 2752-18
CURRENT APPLICATION NUMBER: US/08/635,886C
PRIOR FILING DATE: 1996-04-25
PRIOR APPLICATION NUMBER: PCT/EP94/03555
PRIOR FILING DATE: 1994-10-28
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR FILING DATE: 1993-11-04

NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patent in version 3.1
SEQ ID NO 206
LENGTH: 319
TYPE: PRT
ORGANISM: hepatitis C virus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (319)..(319)
OTHER INFORMATION: Xaa is any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (319)..(319)
OTHER INFORMATION: Xaa is any amino acid
US-08-635-886C-206

Query Match 91.5%; Score 43; DB 2; Length 319;
Best Local Similarity 88.9%; Pred. No. 0.81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
| | | | | | | |
DB 132 DLMGYIPV 140

RESULT 34

US-08-635-886C-217
Sequence 217, Application US/08635886C
Patent No. 6555114
GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, Robert
APPLICANT: MAERTENS, Geert
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
FILE REFERENCE: 2752-18
CURRENT APPLICATION NUMBER: US/08/635,886C
PRIOR FILING DATE: 1996-04-25
PRIOR APPLICATION NUMBER: PCT/EP94/03555
PRIOR FILING DATE: 1994-10-28
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patent in version 3.1
SEQ ID NO 217
LENGTH: 319
TYPE: PRT
ORGANISM: hepatitis C virus
US-08-635-886C-217

Query Match 91.5%; Score 43; DB 2; Length 319;
Best Local Similarity 88.9%; Pred. No. 0.81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
| | | | | | | |
DB 132 DLMGYIPV 140

RESULT 35

US-08-635-886C-228
Sequence 228, Application US/08635886C
Patent No. 6555114
GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, Robert
APPLICANT: MAERTENS, Geert
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
FILE REFERENCE: 2752-18
CURRENT APPLICATION NUMBER: US/08/635,886C
CURRENT FILING DATE: 1996-04-25
PRIOR APPLICATION NUMBER: PCT/EP94/03555

; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 228
; LENGTH: 319
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-228

Query Match 91.5%; Score 43; DB 2; Length 319;
Best Local Similarity 88.9%; Pred. No. 0.81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
||| |||||
Db 132 DLMGYIPV 140

RESULT 36
US-08-635-886C-230

; Sequence 230, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 230
; LENGTH: 319
; TYPE: PRT
; ORGANISM: hepatitis C virus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (144)..(144)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (149)..(149)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (156)..(157)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (161)..(161)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (167)..(167)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (171)..(172)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (174)..(174)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE

; LOCATION: (177)..(177)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (232)..(232)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (233)..(233)
; OTHER INFORMATION: Xaa is any amino acid
US-08-635-886C-230

Query Match 91.5%; Score 43; DB 2; Length 319;
Best Local Similarity 88.9%; Pred. No. 0.81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
||| |||||
Db 132 DLMGYIPV 140

RESULT 37

US-08-974-690C-202
; Sequence 202, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 319
; TYPE: PRT
; ORGANISM: hepatitis C virus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (319)..(319)
; OTHER INFORMATION: Xaa is any amino acid
US-08-974-690C-202

Query Match 91.5%; Score 43; DB 2; Length 319;
Best Local Similarity 88.9%; Pred. No. 0.81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
||| |||||
Db 132 DLMGYIPV 140

RESULT 38

US-08-974-690C-206
; Sequence 206, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555

; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 206
; LENGTH: 319
; TYPE: PRT
; ORGANISM: hepatitis C virus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (131)..(131)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (319)..(319)
; OTHER INFORMATION: Xaa is any amino acid
US-08-974-690C-206

Query Match 91.5%; Score 43; DB 2; Length 319;
Best Local Similarity 88.9%; Pred. No. 0.81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
||| ||| |||
Db 132 DLMGYIPV 140

RESULT 39

US-08-974-690C-217
; Sequence 217, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 217
; LENGTH: 319
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-217

Query Match 91.5%; Score 43; DB 2; Length 319;
Best Local Similarity 88.9%; Pred. No. 0.81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
||| ||| |||
Db 132 DLMGYIPV 140

RESULT 40

US-08-974-690C-228
; Sequence 228, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94

; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 228
; LENGTH: 319
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-228

Query Match 91.5%; Score 43; DB 2; Length 319;
Best Local Similarity 88.9%; Pred. No. 0.81;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
||| ||| |||
Db 132 DLMGYIPV 140

Search completed: January 20, 2006, 22:42:33
Job time : 24 secs

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OM protein - protein search, using sw model

Run on:      January 20, 2006, 22:42:04 ; Search time 30 Seconds
           (without alignments)
           3.040 Million cell updates/sec

Title:      US-10-770-117-1
Perfect score: 47
Sequence:    1 DLMGYIPAV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:    70506 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 70506

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 100 summaries

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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result  No.    Score    Match    Length    DB    ID    Description
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1      42      89.4    2280    7    US-11-022-562-211    Sequence 211, Appl
2      42      89.4    3011    6    US-10-985-205-3      Sequence 3, Appli
3      35      74.5    777     6    US-10-467-657-2474   Sequence 2474, Ap
4      34      72.3    478     6    US-10-873-528-55     Sequence 55, Appl
5      31      66.0    415     6    US-10-467-657-7774   Sequence 7774, Ap
6      31      66.0    502     7    US-11-122-144-12     Sequence 12, Appl
7      30      63.8    103     6    US-10-986-501-169     Sequence 169, App
8      30      63.8    121     6    US-10-793-626-1446    Sequence 1446, Ap
9      30      63.8    130     7    US-11-055-822-156     Sequence 156, App
10     30      63.8    146     6    US-10-793-626-802     Sequence 802, App
11     30      63.8    356     7    US-11-075-185-16      Sequence 16, Appl
12     30      63.8    433     7    US-11-055-822-154     Sequence 154, App
13     29      61.7    80      6    US-10-467-657-5282    Sequence 5282, Ap
14     29      61.7    417     6    US-10-467-657-6612    Sequence 6612, Ap
15     29      61.7    463     6    US-10-467-657-4228    Sequence 4228, Ap
16     29      61.7    769     7    US-11-188-743-15      Sequence 15, Appl
17     29      61.7    1008    7    US-11-055-822-312     Sequence 312, App
18     29      61.7    1152    7    US-11-055-822-308     Sequence 308, App
19     28      59.6    128     6    US-10-467-657-2492    Sequence 2492, Ap
20     28      59.6    160     7    US-10-467-657-12      Sequence 12, Appl
21     28      59.6    168     7    US-11-010-874-7       Sequence 7, Appli
22     28      59.6    257     6    US-10-467-962B-73     Sequence 73, Appl
23     28      59.6    268     7    US-11-055-822-314     Sequence 314, App
24     28      59.6    312     7    US-11-019-711-108     Sequence 108, App
25     28      59.6    332     6    US-10-467-657-4026    Sequence 4026, Ap

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26      28      59.6    339     7    US-11-010-874-2       Sequence 2, Appli
27      28      59.6    380     6    US-10-525-674-28      Sequence 28, Appl
28      28      59.6    411     7    US-10-467-657-8252    Sequence 8252, Ap
29      28      59.6    550     7    US-11-184-380-14      Sequence 14, Appl
30      28      59.6    603     6    US-10-770-726-75      Sequence 75, Appl
31      28      59.6    610     7    US-11-184-380-3       Sequence 3, Appli
32      28      59.6    774     7    US-11-077-886-34      Sequence 34, Appl
33      28      59.6    775     6    US-10-795-201-1       Sequence 1, Appli
34      28      59.6    801     6    US-10-467-657-6470    Sequence 6470, Ap
35      28      59.6    812     7    US-11-010-874-1       Sequence 1, Appli
36      28      59.6    904     6    US-10-967-648A-14     Sequence 14, Appl
37      28      59.6    919     6    US-10-063-703-70      Sequence 70, Appl
38      28      59.6    919     7    US-11-102-240-70      Sequence 70, Appl
39      28      59.6    1010    7    US-11-052-554A-89     Sequence 89, Appl
40      28      59.6    1192    6    US-10-858-730-72      Sequence 72, Appl
41      28      59.6    1206    6    US-10-858-730-73      Sequence 73, Appl
42      28      59.6    1221    6    US-10-858-730-222     Sequence 222, App
43      28      59.6    4128    6    US-10-770-726-77      Sequence 77, Appl
44      27.5    58.5    739     7    US-11-082-389-94      Sequence 94, Appl
45      27.5    58.5    117     7    US-11-103-937-74      Sequence 74, Appl
46      27      57.4    195     6    US-10-957-569-6       Sequence 6, Appli
47      27      57.4    207     6    US-10-467-657-314     Sequence 314, App
48      27      57.4    207     6    US-10-467-657-3272    Sequence 3272, Ap
49      27      57.4    209     6    US-10-995-561-1023    Sequence 1023, Ap
50      27      57.4    292     7    US-11-082-389-342     Sequence 342, App
51      27      57.4    321     6    US-10-485-517-133     Sequence 133, App
52      27      57.4    348     6    US-10-617-034A-1      Sequence 1, Appli
53      27      57.4    375     6    US-10-793-626-1064    Sequence 1064, Ap
54      27      57.4    375     6    US-10-454-437-342     Sequence 342, App
55      27      57.4    394     6    US-10-878-556A-50     Sequence 50, Appl
56      27      57.4    400     6    US-10-821-234-1534    Sequence 1534, Ap
57      27      57.4    530     6    US-10-858-730-67      Sequence 67, Appl
58      27      57.4    552     6    US-10-467-657-4142    Sequence 4142, Ap
59      27      57.4    553     7    US-11-205-109-25      Sequence 25, Appl
60      27      57.4    621     7    US-11-184-380-26      Sequence 26, Appl
61      27      57.4    622     6    US-10-055-877-239     Sequence 239, App
62      27      57.4    635     6    US-10-055-877-67      Sequence 67, Appl
63      27      57.4    693     6    US-10-467-657-6176    Sequence 6176, Ap
64      27      57.4    701     6    US-10-055-877-65      Sequence 65, Appl
65      27      57.4    772     7    US-11-147-238-2       Sequence 2, Appli
66      27      57.4    772     7    US-11-147-238-5       Sequence 5, Appli
67      27      57.4    833     6    US-10-667-295-102     Sequence 102, App
68      27      57.4    839     6    US-10-667-295-101     Sequence 101, App
69      27      57.4    885     6    US-10-055-877-240     Sequence 240, App
70      27      57.4    885     6    US-10-055-877-241     Sequence 241, App
71      27      57.4    886     6    US-10-821-234-1390    Sequence 1390, Ap
72      27      57.4    910     6    US-10-131-826A-112    Sequence 112, App
73      27      57.4    1196    6    US-10-667-295-100     Sequence 100, App
74      27      57.4    1473    7    US-11-019-711-112     Sequence 112, App
75      27      57.4    1508    7    US-11-043-889-47      Sequence 47, Appl
76      27      57.4    2036    7    US-11-124-368A-276    Sequence 276, App
77      27      57.4    2036    7    US-11-124-368A-280    Sequence 280, App
78      27      57.4    2036    7    US-11-124-368A-281    Sequence 281, App
79      27      57.4    2043    7    US-11-124-368A-278    Sequence 278, App
80      27      57.4    2144    7    US-11-124-368A-277    Sequence 277, App
81      27      57.4    2197    7    US-11-075-185-8       Sequence 8, Appli
82      26      55.3    54      6    US-10-927-641-130     Sequence 130, App
83      26      55.3    108     5    US-09-978-360A-440    Sequence 440, App
84      26      55.3    128     7    US-11-116-144-122     Sequence 122, App
85      26      55.3    129     7    US-11-116-144-119     Sequence 119, App
86      26      55.3    177     6    US-10-793-626-2532    Sequence 2532, Ap
87      26      55.3    215     6    US-10-980-388-103     Sequence 103, App
88      26      55.3    219     6    US-10-793-626-221     Sequence 221, Appl
89      26      55.3    229     6    US-10-793-626-2818    Sequence 2818, Ap
90      26      55.3    230     5    US-09-978-360A-698    Sequence 698, App
91      26      55.3    230     6    US-10-131-826A-492    Sequence 492, App
92      26      55.3    230     6    US-10-063-703-80      Sequence 80, Appl
93      26      55.3    230     7    US-11-102-240-80      Sequence 80, Appl
94      26      55.3    230     7    US-11-186-284-24      Sequence 24, Appl
95      26      55.3    258     6    US-10-467-657-1154    Sequence 1154, Ap
96      26      55.3    265     6    US-10-793-626-174     Sequence 174, App
97      26      55.3    267     6    US-10-873-528-114     Sequence 114, App
98      26      55.3    300     7    US-11-055-822-536     Sequence 536, App

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99 26 55.3 300 7 US-11-055-822-630 Sequence 630, App
100 26 55.3 301 6 US-10-995-793-75 Sequence 75, Appl

ALIGNMENTS

RESULT 1

US-11-022-562-211

; Sequence 211, Application US/11022562

; Publication No. US20050249742A1

; GENERAL INFORMATION:

; APPLICANT: Ruprecht, Ruth M.

; APPLICANT: Shisong, Jiang

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING

; FILE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE

; FILE REFERENCE: DFN-043CN

; CURRENT APPLICATION NUMBER: US/11/022,562

; CURRENT FILING DATE: 2004-12-22

; PRIOR APPLICATION NUMBER: PCT/US03/20322

; PRIOR FILING DATE: 2003-06-27

; PRIOR APPLICATION NUMBER: 60/392718

; PRIOR FILING DATE: 2002-06-27

; NUMBER OF SEQ ID NOS: 340

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 211

; LENGTH: 2280

; TYPE: PRT

; ORGANISM: Hepatitis C Virus

US-11-022-562-211

Query Match

Best Local Similarity 89.4%; Score 42; DB 7; Length 2280;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9

Db 132 DLMGYIPLV 140

RESULT 2

US-10-985-205-3

; Sequence 3, Application US/10985205

; Publication No. US20050266400A1

; GENERAL INFORMATION:

; APPLICANT: Dumonceaux, Julie

; APPLICANT: Cormier, Emmanuel G.

; APPLICANT: Gardner, Jason P.

; APPLICANT: Dragic, Tatjana

; TITLE OF INVENTION: NOVEL SEQUENCES ENCODING HEPATITIS C VIRUS GLYCOPROTEINS

; FILE REFERENCE: 71242-A/JPW/AUD

; CURRENT APPLICATION NUMBER: US/10/985,205

; CURRENT FILING DATE: 2004-11-09

; PRIOR APPLICATION NUMBER: US 60/519,536

; PRIOR FILING DATE: 2003-11-12

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 3011

; TYPE: PRT

; ORGANISM: Hepatitis C virus

US-10-985-205-3

Query Match

Best Local Similarity 89.4%; Score 42; DB 6; Length 3011;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9

Db 132 DLMGYIPLV 140

RESULT 3

US-10-467-657-2474

; Sequence 2474, Application US/10467657

; Publication No. US20050260581A1

; GENERAL INFORMATION:

; APPLICANT: CHIRON Spa

; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariagrazia

; APPLICANT: MASIGNANI Vega

; APPLICANT: MONACI Elisabetta

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218

; SOFTWARE: SeqWin99, version 1.04

; SEQ ID NO 2474

; LENGTH: 777

; TYPE: PRT

; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-2474

Query Match

Best Local Similarity 74.5%; Score 35; DB 6; Length 777;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPA 8

Db 221 DLMGYIPA 228

RESULT 4

US-10-873-528-55

; Sequence 55, Application US/10873528

; Publication No. US20050276814A1

; GENERAL INFORMATION:

; APPLICANT: Microbial Technics Limited

; APPLICANT: Gilbert, Christophe FG

; APPLICANT: Hansbro, Philip M

; TITLE OF INVENTION: Proteins

; FILE REFERENCE: PWC/P21129WO

; CURRENT APPLICATION NUMBER: US/10/873,528

; CURRENT FILING DATE: 2004-06-23

; PRIOR APPLICATION NUMBER: US/09/769,787

; PRIOR FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: GB 9816337.1

; PRIOR FILING DATE: 1998-03-27

; PRIOR APPLICATION NUMBER: US 60/125164

; PRIOR FILING DATE: 1999-03-19

; NUMBER OF SEQ ID NOS: 388

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 55

; LENGTH: 478

; TYPE: PRT

; ORGANISM: Streptococcus pneumoniae

US-10-873-528-55

Query Match

Best Local Similarity 72.3%; Score 34; DB 6; Length 478;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIP 7

Db 416 DLMGYTP 422

RESULT 5

US-10-467-657-7774

; Sequence 7774, Application US/10467657

; Publication No. US20050260581A1

; GENERAL INFORMATION:

; APPLICANT: CHIRON Spa

APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 7774
LENGTH: 415
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7774

Query Match 66.0%; Score 31; DB 6; Length 415;
Best Local Similarity 71.4%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIP 7
|||
DB 327 DLTGYLP 333

RESULT 6
US-11-122-144-12
Sequence 12, Application US/11122144
Publication No. US20050287663A1
GENERAL INFORMATION:
APPLICANT: Gillespie, Alison
Claeys, Brian O.
Chavez-Noriega, Laura Elena
Siegel, Robert
Elliot, Kathryn J.
TITLE OF INVENTION: DNA ENCODING HUMAN (AND (SUBUNITS
OF NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR, CELLS TRANSFORMED THEREWITH,
AND RECOMBINANT CELL LINE EXPRESSING

NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/122,144
FILING DATE: 04-May-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/703,951
FILING DATE: 01-Nov-2000
APPLICATION NUMBER: US 08/487,596
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: WO US94/02447
FILING DATE: 08-MAR-1994
APPLICATION NUMBER: US 08/149,503
FILING DATE: 08-NOV-1993
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
APPLICATION NUMBER: US 07/938,154
FILING DATE: 30-NOV-1992
APPLICATION NUMBER: US 07/504,455
FILING DATE: 03-APR-1990

ATTORNEY/AGENT INFORMATION:
NAME: Kohl, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: SD99511A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3889
TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-11-122-144-12

Query Match 66.0%; Score 31; DB 7; Length 502;
Best Local Similarity 71.4%; Pred. No. 45;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIP 7
|||
DB 186 DISGYIP 192

RESULT 7
US-10-986-501-169
Sequence 169, Application US/10986501
Publication No. US20050244845A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: PZ013P2C1
CURRENT APPLICATION NUMBER: US/10/986.501
CURRENT FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: US/10/621,363
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/969,730
PRIOR FILING DATE: 2001-10-06
PRIOR APPLICATION NUMBER: 09/774,639
PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/238,291
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: PCT/US98/16235
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,366
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,364
PRIOR FILING DATE: 1997-08-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 373
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 169
LENGTH: 103
TYPE: PRT
ORGANISM: Homo sapiens
US-10-986-501-169

Query Match 63.8%; Score 30; DB 6; Length 103;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 MGYIPAV 9
|||
DB 21 MGYIPVL 27

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RESULT 8
US-10-793-626-1446
; Sequence 1446, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1446
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1446

Query Match          63.8%; Score 30; DB 6; Length 121;
Best Local Similarity 62.5%; Pred. No. 14; Mismatches 2; Indels 1; Gaps 0;
Matches 5; Conservative 2;

QY      2 LMGYIPAV 9
      |:||||:
Db      30 LIGYIPPI 37

RESULT 9
US-11-055-822-156
; Sequence 156, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 156
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
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US-11-055-822-156

Query Match          63.8%; Score 30; DB 7; Length 130;
Best Local Similarity 83.3%; Pred. No. 15; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY      4 GYIPAV 9
      |:||||:
Db      26 GYLPAV 31

RESULT 10
US-10-793-626-802
; Sequence 802, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 802
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-802

Query Match          63.8%; Score 30; DB 6; Length 146;
Best Local Similarity 55.6%; Pred. No. 18; Mismatches 3; Indels 1; Gaps 0;
Matches 5; Conservative 3;

QY      1 DLMGYIPAV 9
      |:||||:
Db      103 DIIGYIEM 111

RESULT 11
US-11-075-185-16
; Sequence 16, Application US/11075185
; Publication No. US20050266434A1
; GENERAL INFORMATION:
; APPLICANT: REEVES, CHRISTOPHER D
; APPLICANT: JULIEN, BRYAN
; APPLICANT: REID, RALPH
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
; FILE REFERENCE: 010099.03
; CURRENT APPLICATION NUMBER: US/11/075,185
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/551,103
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US 60/568,290
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-11-075-185-16

Query Match          63.8%; Score 30; DB 7; Length 356;
Best Local Similarity 62.5%; Pred. No. 49; Mismatches 1; Indels 2; Gaps 0;
Matches 5; Conservative 1;

QY      1 DLMGYIPA 8
      |:||||:
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Db      121 DAEGYVPA 128

RESULT 12
US-11-055-822-154
; Sequence 154, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 154
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-154

Query Match      63.8%; Score 30; DB 7; Length 433;
Best Local Similarity 83.3%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 GYIPAV 9
Db      26 GYLPAV 31

RESULT 13
US-10-467-657-5282
; Sequence 5282, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 154
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5282

Query Match      61.7%; Score 29; DB 6; Length 417;
Best Local Similarity 71.4%; Pred. No. 95;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LMGYVPA 8
Db      197 LMGMWPA 203

RESULT 14
US-10-467-657-6612
; Sequence 6612, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6612
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6612

Query Match      61.7%; Score 29; DB 6; Length 417;
Best Local Similarity 71.4%; Pred. No. 95;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LMGYVPA 8
Db      197 LMGMWPA 203

RESULT 15
US-10-467-657-4228
; Sequence 4228, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4228
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4228

Query Match      61.7%; Score 29; DB 6; Length 463;
```

Best Local Similarity 71.4%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 1;

Qy 1 DLMGYIP 7
||| |:
Db 23 DLMRYLP 29

RESULT 16
US-11-188-743-15
; Sequence 15, Application US/11188743
; Publication No. US20050272140A1
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas
; APPLICANT: Sasse, Philip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Grasso, Luigi
; APPLICANT: Vogelstein, Bart
; TITLE OF INVENTION: Methods for generating hypermutable
; TITLE OF INVENTION: Yeast
; FILE REFERENCE: 01107.00097
; CURRENT APPLICATION NUMBER: US/11/188,743
; CURRENT FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: US/10/641,068
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US/09/788,657
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,336
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-11-188-743-15

Query Match 61.7%; Score 29; DB 7; Length 769;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LMGYIPAV 9
| |||||:
Db 656 LKGYP SL 663

RESULT 17
US-11-055-822-312
; Sequence 312, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 308
; LENGTH: 1152
; TYPE: PRT

; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 312
; LENGTH: 1008
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (181)..(182)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 183
; OTHER INFORMATION: Xaa = Phe, Leu, Ile, or Val
US-11-055-822-312

Query Match 61.7%; Score 29; DB 7; Length 1008;
Best Local Similarity 55.6%; Pred. No. 2.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
| | | | |:
Db 390 ELLLYP AV 398

RESULT 18
US-11-055-822-308
; Sequence 308, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 308
; LENGTH: 1152
; TYPE: PRT

ORGANISM: Corynebacterium glutamicum
US-11-055-822-308

Query Match 61.7%; Score 29; DB 7; Length 1152;
Best Local Similarity 55.6%; Pred. No. 3.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 390 ELLLYVFAV 398
:|:|:|

RESULT 19
US-10-467-657-2492
; Sequence 2492, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2492
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2492

Query Match 59.6%; Score 28; DB 6; Length 128;
Best Local Similarity 42.9%; Pred. No. 40;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLMGYIP 7
Db 63 DIIGFVP 69
|:|:|

RESULT 20
US-11-010-874-12
; Sequence 12, Application US/11010874
; Publication No. US20050250694A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Jian-Xing
; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
; TITLE OF INVENTION: FIBROSIS AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: 5820.656
; CURRENT APPLICATION NUMBER: US/11/010,874
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 10/963,115
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/510,620
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/528,647
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 160
; TYPE: PRT
; ORGANISM: murine
US-11-010-874-12

Query Match 59.6%; Score 28; DB 7; Length 160;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYIPA 8
Db 116 GYIPA 120
|:|:|

RESULT 21
US-11-010-874-7
; Sequence 7, Application US/11010874
; Publication No. US20050250694A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Jian-Xing
; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION A
; TITLE OF INVENTION: FIBROSIS AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: 5820.656
; CURRENT APPLICATION NUMBER: US/11/010,874
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 10/963,115
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/510,620
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/528,647
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 168
; TYPE: PRT
; ORGANISM: murine
US-11-010-874-7

Query Match 59.6%; Score 28; DB 7; Length 168;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYIPA 8
Db 34 GYIPA 38
|:|:|

RESULT 22
US-10-467-962B-73
; Sequence 73, Application US/10467962B
; Publication No. US20050246784A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Blau, Astrid
; APPLICANT: Daeschner, Klaus
; APPLICANT: Klein, Mathieu
; TITLE OF INVENTION: Identification of Herbicidally Active Substances
; FILE REFERENCE: 2000_857
; CURRENT APPLICATION NUMBER: US/10/467,962B
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/EP02/01466
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn vers. 2.0
; SEQ ID NO 73
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-467-962B-73

Query Match 59.6%; Score 28; DB 6; Length 257;
Best Local Similarity 83.3%; Pred. No. 88;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLMGYI 6
Db 153 DLVGVI 158
|:|:|

RESULT 23

```
US-11-055-822-314
; Sequence 314, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Krogger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberkauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 314
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-314

Query Match 59.6%; Score 28; DB 7; Length 268;
Best Local Similarity 66.7%; Pred. No. 93;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
   :| | | | |
Db 42 ELTGSIPIAV 50

RESULT 24
US-11-019-711-108
; Sequence 108, Application US/11019711
; Publication No. US2006009634A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark

US-10-467-657-4026
; Sequence 4026, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4026
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4026

Query Match 59.6%; Score 28; DB 7; Length 312;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPA 8
   :| | | |
Db 26 BIPGYLPA 33

RESULT 25
US-10-467-657-4026
; Sequence 4026, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4026
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4026
```

```
Query Match          59.6%; Score 28; DB 6; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GYIPA 8
      |||||
Db      79 GYIPA 83

RESULT 26
US-11-010-874-2
; Sequence 2, Application US/11010874
; Publication No. US20050250694A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Jian-Xing
; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
; FILE OF INVENTION: FIBROSIS AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: 5820.656
; CURRENT APPLICATION NUMBER: US/11/010,874
; CURRENT FILING DATE: 2004-12-13
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/510,620
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/528,647
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 339
; TYPE: PRT
; ORGANISM: murine
US-11-010-874-2

Query Match          59.6%; Score 28; DB 7; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GYIPA 8
      |||||
Db      121 GYIPA 125

RESULT 27
US-10-525-674-28
; Sequence 28, Application US/10525674
; Publication No. US20060003425A1
; GENERAL INFORMATION:
; APPLICANT: Kroger, Burkhard
; APPLICANT: Zelder, Oskar
; APPLICANT: Kolprogge, Corinna
; APPLICANT: Schroder, Hartwig
; APPLICANT: Hafner, Stefan
; TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals Containing
; FILE OF INVENTION: Sulphur (Meta)
; FILE REFERENCE: 13111-00002-US
; CURRENT APPLICATION NUMBER: US/10/525,674
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: PCT/EP 2003/009452
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: DE 102 39 073.8
; PRIOR FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Thermus thermophilus
US-10-525-674-28

Query Match          59.6%; Score 28; DB 6; Length 380;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;

QY      4 GYIPA 8
      |||||
Db      148 GYIPA 152

Query Match          59.6%; Score 28; DB 6; Length 411;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 MGYP 7
      |||||
Db      375 MGYP 379

RESULT 29
US-11-184-380-14
; Sequence 14, Application US/11184380
; Publication No. US20050255089A1
; GENERAL INFORMATION:
; APPLICANT: Chlorini, John
; APPLICANT: Kotin, Robert M.
; TITLE OF INVENTION: AAV5 NUCLEIC ACIDS
; FILE REFERENCE: 14014.0323U3
; CURRENT APPLICATION NUMBER: US/11/184,380
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: PCT/US99/11958
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,029
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Note =
; OTHER INFORMATION: synthetic construct
US-11-184-380-14

Query Match          59.6%; Score 28; DB 7; Length 550;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GYIPA 8
      |||||
Db      148 GYIPA 152
```

```

; APPLICANT: Frey, Bruno
; APPLICANT: Antranikian, Garabed
; APPLICANT: Boehlke, Kristina
; APPLICANT: Plesni, Francesca Maria
; APPLICANT: Rossi, Mose
; TITLE OF INVENTION: Mutant B-type DNA Polymerases Exhibiting Improved Performance i
; FILE REFERENCE: 5328
; CURRENT APPLICATION NUMBER: US/11/077,886
; CURRENT FILING DATE: 2005-03-11
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: EP/00105155.6
; PRIOR FILING DATE: 2000-03-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 774
; TYPE: PRT
; ORGANISM: T. aggregans
US-11-077-886-34

Query Match          59.6%; Score 28; DB 7; Length 774;
Best Local Similarity 44.4%; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
|:|:|:|:|
Db 447 DPGFIPSI 455

RESULT 33
US-10-795-201-1
; Sequence 1, Application US/10795201
; Publication No. US20050282171A1
; GENERAL INFORMATION:
; APPLICANT: Mathur, Eric J
; TITLE OF INVENTION: PURIFIED THERMOSTABLE PYROCOCCLUS FURIOSUS DNA
; FILE REFERENCE: 4121.0004-06
; CURRENT APPLICATION NUMBER: US/10/795,201
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US/10/176,357
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US 09/244,889
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 07/803,627
; PRIOR FILING DATE: 1991-12-02
; PRIOR APPLICATION NUMBER: US 07/776,552
; PRIOR FILING DATE: 1991-10-15
; PRIOR APPLICATION NUMBER: US 07/657,073
; PRIOR FILING DATE: 1991-02-19
; PRIOR APPLICATION NUMBER: US 07/620,568
; PRIOR FILING DATE: 1990-12-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Pyrococcus furiosus
US-10-795-201-1

Query Match          59.6%; Score 28; DB 6; Length 775;
Best Local Similarity 44.4%; Pred. No. 3.2e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
|:|:|:|:|
Db 445 DIPGFIPSL 453

RESULT 34
US-10-467-657-6470
; Sequence 6470, Application US/10467657
; APPLICANT: Sobek, Harald
; APPLICANT: Wyeth
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-0100000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-75

Query Match          59.6%; Score 28; DB 6; Length 603;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYIPA 8
|:|:|:|
Db 308 GYIPA 312

RESULT 31
US-11-184-380-3
; Sequence 3, Application US/11184380
; Publication No. US20050255089A1
; GENERAL INFORMATION:
; APPLICANT: Chiorini, John
; APPLICANT: Kotin, Robert M.
; TITLE OF INVENTION: AAVS NUCLEIC ACIDS
; FILE REFERENCE: 14014.032303
; CURRENT APPLICATION NUMBER: US/11/184,380
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: PCT/US99/11958
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,029
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Note =
; OTHER INFORMATION: synthetic construct
US-11-184-380-3

Query Match          59.6%; Score 28; DB 7; Length 610;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYIPA 8
|:|:|:|
Db 148 GYIPA 152

RESULT 32
US-11-077-886-34
; Sequence 34, Application US/11077886
; Publication No. US20050266436A1
; GENERAL INFORMATION:
; APPLICANT: Sobek, Harald
```

; Publication No. US20050360581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6470
; LENGTH: 801
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6470

Query Match 59.6%; Score 28; DB 6; Length 801;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GVIPA 8
Db 786 GVIPA 790
|||||

RESULT 35

US-11-010-874-1
; Sequence 1, Application US/11010874
; Publication No. US20050250694A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Jian-King
; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
; FILE REFERENCE: 5820.636
; CURRENT APPLICATION NUMBER: US/11/010,874
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 10/963,115
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/510,620
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/528,647
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 812
; TYPE: PRT
; ORGANISM: murine
US-11-010-874-1

Query Match 59.6%; Score 28; DB 7; Length 812;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GVIPA 8
Db 218 GVIPA 222
|||||

RESULT 36

US-10-967-648A-14
; Sequence 14, Application US/10967648A
; Publication No. US20050245473A1
; GENERAL INFORMATION:
; APPLICANT: Saunders, Nicholas A
; TITLE OF INVENTION: Differentiation- and/or proliferation-modulating agents and uses
; FILE REFERENCE: 12493972

; CURRENT APPLICATION NUMBER: US/10/967,648A
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: USSN 60/512010
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 904
; TYPE: PRT
; ORGANISM: Mouse
US-10-967-648A-14

Query Match 59.6%; Score 28; DB 6; Length 904;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLMGY 5
Db 245 DLMGY 249
|||||

RESULT 37

US-10-063-703-70
; Sequence 70, Application US/10063703
; Publication No. US2006008901A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,703
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 70
; LENGTH: 919
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-703-70

Query Match 59.6%; Score 28; DB 6; Length 919;
Best Local Similarity 50.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LMGYIPAV 9
Db 618 LMGYIPVL 625
|||||

RESULT 38

US-11-102-240-70
; Sequence 70, Application US/11102240
; Publication No. US20050260647A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRES
; FILE REFERENCE: P3230R1C106C
; CURRENT APPLICATION NUMBER: US/11/102,240
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 10/063662

; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 199-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 70
; LENGTH: 919
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-102-240-70

Query Match 59.6%; Score 28; DB 7; Length 919;
Best Local Similarity 50.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LMGYIPAV 9
Db 618 LOGYVPVL 625

RESULT 39

US-11-052-554A-89
; Sequence 89, Application US/11052554A
; Publication No. US2005028866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; PRIOR FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 89
; LENGTH: 1010
; TYPE: PRT
; ORGANISM: Haemophilus influenzae Rd
US-11-052-554A-89

Query Match 59.6%; Score 28; DB 7; Length 1010;
Best Local Similarity 44.4%; Pred. No. 4.3e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 941 DLIGYVPI 949

RESULT 40

US-10-858-730-72
; Sequence 72, Application US/10858730
; Publication No. US2005025568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; FILE REFERENCE: 14184-030001

; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-858-730-72

Query Match 59.6%; Score 28; DB 6; Length 1192;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GYIPAV 9
Db 995 GYFPVAV 1000

Search completed: January 20, 2006, 22:53:10
Job time : 31 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 20, 2006, 22:24:52 ; Search time 70 Seconds

(without alignments)
90.711 Million cell updates/sec

Title: US-10-770-117-1

Perfect score: 47

Sequence: 1 DLMGYIPAV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Uniprot_05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	91.5	136	2	Q7TLE8_9HEPC
2	43	91.5	137	2	Q7TLG1_9HEPC
3	43	91.5	137	2	Q7TLG2_9HEPC
4	43	91.5	137	2	Q7TLG3_9HEPC
5	43	91.5	137	2	Q7TLG4_9HEPC
6	43	91.5	137	2	Q7TLG5_9HEPC
7	43	91.5	137	2	Q7TLG6_9HEPC
8	43	91.5	137	2	Q7TLG7_9HEPC
9	43	91.5	137	2	Q7TLG8_9HEPC
10	43	91.5	167	2	Q5UBV2_9HEPC
11	43	91.5	188	2	O09740_9HEPC
12	43	91.5	191	2	Q68411_9HEPC
13	43	91.5	191	2	Q8BES0_9HEPC
14	43	91.5	191	2	Q8JW46_9HEPC
15	43	91.5	191	2	Q68107_9HEPC
16	43	91.5	191	2	Q68112_9HEPC
17	43	91.5	191	2	Q68115_9HEPC
18	43	91.5	191	2	Q68128_9HEPC
19	43	91.5	191	2	Q68141_9HEPC
20	43	91.5	191	2	Q68143_9HEPC
21	43	91.5	191	2	Q68146_9HEPC
22	43	91.5	191	2	Q68147_9HEPC
23	43	91.5	191	2	Q68150_9HEPC
24	43	91.5	191	2	Q68150_9HEPC
25	43	91.5	191	2	Q68109_9HEPC
26	43	91.5	192	2	Q68711_9HEPC
27	43	91.5	193	2	Q68709_9HEPC
28	43	91.5	193	2	Q81558_9HEPC
29	43	91.5	195	2	Q91TF6_9HEPC
30	43	91.5	235	2	Q68692_9HEPC
31	43	91.5	235	2	Q68694_9HEPC

32	43	91.5	313	2	Q68687_9HEPC	Q68687 hepatitis c
33	43	91.5	317	2	Q68689_9HEPC	Q68689 hepatitis c
34	43	91.5	317	2	Q68696_9HEPC	Q68696 hepatitis c
35	43	91.5	317	2	Q68663_9HEPC	Q68663 hepatitis c
36	43	91.5	318	2	Q68691_9HEPC	Q68691 hepatitis c
37	43	91.5	318	2	Q81262_9HEPC	Q81262 hepatitis c
38	43	91.5	319	2	Q68678_9HEPC	Q68678 hepatitis c
39	43	91.5	319	2	Q68688_9HEPC	Q68688 hepatitis c
40	43	91.5	319	2	Q68693_9HEPC	Q68693 hepatitis c
41	43	91.5	319	2	Q68695_9HEPC	Q68695 hepatitis c
42	43	91.5	319	2	Q68697_9HEPC	Q68697 hepatitis c
43	43	91.5	319	2	Q68699_9HEPC	Q68699 hepatitis c
44	43	91.5	319	2	Q68700_9HEPC	Q68700 hepatitis c
45	43	91.5	319	2	Q68701_9HEPC	Q68701 hepatitis c
46	43	91.5	319	2	Q68702_9HEPC	Q68702 hepatitis c
47	43	91.5	319	2	Q68703_9HEPC	Q68703 hepatitis c
48	43	91.5	319	2	Q68705_9HEPC	Q68705 hepatitis c
49	43	91.5	319	2	Q81557_9HEPC	Q81557 hepatitis c
50	43	91.5	414	2	P89962_9HEPC	P89962 hepatitis c
51	43	91.5	414	2	P89963_9HEPC	P89963 hepatitis c
52	43	91.5	414	2	Q68790_9HEPC	Q68790 hepatitis c
53	43	91.5	414	2	Q68804_9HEPC	Q68804 hepatitis c
54	43	91.5	414	2	Q68813_9HEPC	Q68813 hepatitis c
55	43	91.5	414	2	Q68818_9HEPC	Q68818 hepatitis c
56	43	91.5	414	2	Q81267_9HEPC	Q81267 hepatitis c
57	43	91.5	414	2	Q81268_9HEPC	Q81268 hepatitis c
58	43	91.5	414	2	Q81269_9HEPC	Q81269 hepatitis c
59	43	91.5	414	2	Q81270_9HEPC	Q81270 hepatitis c
60	43	91.5	414	2	Q81271_9HEPC	Q81271 hepatitis c
61	43	91.5	414	2	Q81314_9HEPC	Q81314 hepatitis c
62	43	91.5	414	2	P89956_9HEPC	P89956 hepatitis c
63	43	91.5	414	2	P89960_9HEPC	P89960 hepatitis c
64	43	91.5	414	2	Q81329_9HEPC	Q81329 hepatitis c
65	43	91.5	415	2	P87751_9HEPC	P87751 hepatitis c
66	43	91.5	415	2	P89961_9HEPC	P89961 hepatitis c
67	43	91.5	415	2	P89964_9HEPC	P89964 hepatitis c
68	43	91.5	415	2	P89965_9HEPC	P89965 hepatitis c
69	43	91.5	415	2	Q68791_9HEPC	Q68791 hepatitis c
70	43	91.5	415	2	Q68810_9HEPC	Q68810 hepatitis c
71	43	91.5	415	2	Q68820_9HEPC	Q68820 hepatitis c
72	43	91.5	415	2	Q81640_9HEPC	Q81640 hepatitis c
73	43	91.5	416	2	Q39647_9HEPC	Q39647 hepatitis c
74	43	91.5	506	2	Q80HT3_9HEPC	Q80HT3 hepatitis c
75	43	91.5	508	2	Q80HT4_9HEPC	Q80HT4 hepatitis c
76	43	91.5	514	2	Q6XJ47_9HEPC	Q6XJ47 hepatitis c
77	43	91.5	736	1	POLG_HCVJ5	P27960 hepatitis c
78	43	91.5	736	1	POLG_HCVJ7	P27961 hepatitis c
79	43	91.5	874	2	Q7LZY5_9HEPC	Q7LZY5 hepatitis c
80	43	91.5	874	2	Q7LZY6_9HEPC	Q7LZY6 hepatitis c
81	43	91.5	1123	2	Q8QP51_9HEPC	Q8QP51 hepatitis c
82	43	91.5	1130	2	Q8QP50_9HEPC	Q8QP50 hepatitis c
83	43	91.5	3010	2	P88803_9HEPC	P88803 hepatitis c
84	43	91.5	3010	2	P90191_9HEPC	P90191 hepatitis c
85	43	91.5	3013	2	Q92530_9HEPC	Q92530 hepatitis c
86	43	91.5	3014	2	Q6GYR8_9HEPC	Q6GYR8 hepatitis c
87	43	91.5	3015	2	Q9FWU9_9ZZZZ	Q9FWU9 synthetic c
88	43	91.5	3015	2	Q9FWX5_9ZZZZ	Q9FWX5 synthetic c
89	43	91.5	3015	2	Q4QTD9_9HEPC	Q4QTD9 hepatitis c
90	43	91.5	3016	2	Q92531_9HEPC	Q92531 hepatitis c
91	43	91.5	3019	2	Q92529_9HEPC	Q92529 hepatitis c
92	43	91.5	3019	2	Q5I2N3_9HEPC	Q5I2N3 hepatitis c
93	43	91.5	3032	1	POLG_HCVJ6	P26660 h genome po
94	43	91.5	3032	1	POLG_HCVJ8	P26661 h genome po
95	43	91.5	3032	2	Q99IB2_9HEPC	Q99IB2 hepatitis c
96	43	91.5	3032	2	Q99IB4_9HEPC	Q99IB4 hepatitis c
97	43	91.5	3032	2	Q99A9_9HEPC	Q99A9 hepatitis c
98	43	91.5	3033	2	Q99IB3_9HEPC	Q99IB3 hepatitis c
99	43	91.5	3033	2	Q99IB5_9HEPC	Q99IB5 hepatitis c
100	43	91.5	3033	2	Q99IB6_9HEPC	Q99IB6 hepatitis c

ALIGNMENTS

```
RESULT 1
Q7TLG8_9HEPC
ID Q7TLG8_9HEPC PRELIMINARY; PRT; 136 AA.
AC Q7TLG8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;
RA Ndjomou J., Pybus O.G., Matz B.;
RT "Phylogenetic analysis of hepatitis C virus isolates indicates a
unique pattern of endemic infection in Cameroon.";
RL J. Gen. Virol. 84:2333-2341(2003).
DR EMBL; AY256819; AAP34683.1; -; Genomic_RNA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV core.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR NON_TER 1
FT NON_TER 136
SQ SEQUENCE 136 AA; 14878 MW; B3FBG7DDFF37DCOF CRC64;

Query Match 91.5%; Score 43; DB 2; Length 136;
Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 99 DLMGYIPV 107

RESULT 2
Q7TLG1_9HEPC
ID Q7TLG1_9HEPC PRELIMINARY; PRT; 137 AA.
AC Q7TLG1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;
RA Ndjomou J., Pybus O.G., Matz B.;
RT "Phylogenetic analysis of hepatitis C virus isolates indicates a
unique pattern of endemic infection in Cameroon.";
RL J. Gen. Virol. 84:2333-2341(2003).
DR EMBL; AY256806; AAP34670.1; -; Genomic_RNA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR NON_TER 1
FT NON_TER 137
SQ SEQUENCE 137 AA; 14992 MW; 6BD2F278178C5F4D CRC64;

Query Match 91.5%; Score 43; DB 2; Length 137;
Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 99 DLMGYIPV 107

RESULT 3
Q7TLG2_9HEPC
ID Q7TLG2_9HEPC PRELIMINARY; PRT; 137 AA.
AC Q7TLG2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;
RA Ndjomou J., Pybus O.G., Matz B.;
RT "Phylogenetic analysis of hepatitis C virus isolates indicates a
unique pattern of endemic infection in Cameroon.";
RL J. Gen. Virol. 84:2333-2341(2003).
DR EMBL; AY256805; AAP34669.1; -; Genomic_RNA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR NON_TER 1
FT NON_TER 137
SQ SEQUENCE 137 AA; 14992 MW; 6BD2F278178C5F4D CRC64;

Query Match 91.5%; Score 43; DB 2; Length 137;
Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 99 DLMGYIPV 107

RESULT 4
Q7TLG3_9HEPC
ID Q7TLG3_9HEPC PRELIMINARY; PRT; 137 AA.
AC Q7TLG3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;
RA Ndjomou J., Pybus O.G., Matz B.;
RT "Phylogenetic analysis of hepatitis C virus isolates indicates a
unique pattern of endemic infection in Cameroon.";
RL J. Gen. Virol. 84:2333-2341(2003).
DR EMBL; AY256804; AAP34668.1; -; Genomic_RNA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR NON_TER 1
FT NON_TER 137
SQ SEQUENCE 137 AA; 14992 MW; 6BD2F278178C5F4D CRC64;

Query Match 91.5%; Score 43; DB 2; Length 137;
Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 99 DLMGYIPV 107
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SQ SEQUENCE 137 AA; 14992 MW; 6BD2F278178C5F4D CRC64;
Query Match 91.5%; Score 43; DB 2; Length 137;
Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 99 DLMGYIPV 107

RESULT 5
Q7TLG4_9HEPC
ID Q7TLG4_9HEPC PRELIMINARY; PRT; 137 AA.
AC Q7TLG4;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;
RA Ndjomou J., Pybus O.G., Matz B.;
RT "Phylogenetic analysis of hepatitis C virus isolates indicates a
RT unique pattern of endemic infection in Cameroon.";
RL J. Gen. Virol. 84:2333-2341(2003).
DR EMBL; AY256803; AAP34667.1; -; Genomic_RNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV core.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR NON_TER 1
FT NON_TER 137
SQ SEQUENCE 137 AA; 15092 MW; 46BB62E11D92B9DD CRC64;

Query Match 91.5%; Score 43; DB 2; Length 137;
Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 99 DLMGYIPV 107

RESULT 6
Q7TLG5_9HEPC
ID Q7TLG5_9HEPC PRELIMINARY; PRT; 137 AA.
AC Q7TLG5;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;
RA Ndjomou J., Pybus O.G., Matz B.;
RT "Phylogenetic analysis of hepatitis C virus isolates indicates a
RT unique pattern of endemic infection in Cameroon.";
RL J. Gen. Virol. 84:2333-2341(2003).
DR EMBL; AY256802; AAP34666.1; -; Genomic_RNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR NON_TER 1
FT NON_TER 137
SQ SEQUENCE 137 AA; 15092 MW; 46BB62E11D92B9DD CRC64;

Query Match 91.5%; Score 43; DB 2; Length 137;
Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 99 DLMGYIPV 107

RESULT 7
Q7TLG6_9HEPC
ID Q7TLG6_9HEPC PRELIMINARY; PRT; 137 AA.
AC Q7TLG6;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;
RA Ndjomou J., Pybus O.G., Matz B.;
RT "Phylogenetic analysis of hepatitis C virus isolates indicates a
RT unique pattern of endemic infection in Cameroon.";
RL J. Gen. Virol. 84:2333-2341(2003).
DR EMBL; AY256801; AAP34665.1; -; Genomic_RNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR NON_TER 1
FT NON_TER 137
SQ SEQUENCE 137 AA; 14890 MW; 6BD8373BF43909B8 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 137;
Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 99 DLMGYIPV 107

RESULT 8
Q7TLG7_9HEPC
ID Q7TLG7_9HEPC PRELIMINARY; PRT; 137 AA.
AC Q7TLG7;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;
RA Ndjomou J., Pybus O.G., Matz B.;
RT "Phylogenetic analysis of hepatitis C virus isolates indicates a
RT unique pattern of endemic infection in Cameroon.";
DR InterPro; IPR002522; HCV capsid.
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DR InterPro; IPR002521; HCV core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
FT NON_TER 1
FT NON_TER 137
SQ SEQUENCE 137 AA; 15000 MW; D17F9B2D8C78F647 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 137;
Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 99 DLMGYIPV 107

RESULT 7
Q7TLG6_9HEPC
ID Q7TLG6_9HEPC PRELIMINARY; PRT; 137 AA.
AC Q7TLG6;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;
RA Ndjomou J., Pybus O.G., Matz B.;
RT "Phylogenetic analysis of hepatitis C virus isolates indicates a
RT unique pattern of endemic infection in Cameroon.";
RL J. Gen. Virol. 84:2333-2341(2003).
DR EMBL; AY256801; AAP34665.1; -; Genomic_RNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR NON_TER 1
FT NON_TER 137
SQ SEQUENCE 137 AA; 14890 MW; 6BD8373BF43909B8 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 137;
Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 99 DLMGYIPV 107

RESULT 8
Q7TLG7_9HEPC
ID Q7TLG7_9HEPC PRELIMINARY; PRT; 137 AA.
AC Q7TLG7;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;
RA Ndjomou J., Pybus O.G., Matz B.;
RT "Phylogenetic analysis of hepatitis C virus isolates indicates a
RT unique pattern of endemic infection in Cameroon.";
DR InterPro; IPR002522; HCV capsid.
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RP J. Gen. Virol. 84:2333-2341(2003).
RC EMBL; AY256800; AAP34664.1; -; Genomic_RNA.
RA Chub E.V., Shustov A.V., Netesov S.V.;
RT "Intergenotypic recombinants of Hepatitis C virus found in Sough
RT Siberia.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY764170; AAV35986.1; -; Genomic_RNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV core.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV core; 1.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 14962 MW; 6BDB826D178C5F58 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 137;
Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 99 DLMGYIPV 107

RESULT 9
Q7TLG8_9HEPC PRELIMINARY; PRT; 137 AA.
AC Q7TLG8;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=111103;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22798990; PubMed=12917453; DOI=10.1099/vir.0.19240-0;
RA Ndjomou J., Pybus O.G., Matz B.;
RT "Phylogenetic analysis of hepatitis C virus isolates indicates a
RT unique pattern of endemic infection in Cameroon.";
RL J. Gen. Virol. 84:2333-2341(2003).
DR EMBL; AY256799; AAP34663.1; -; Genomic_RNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV core.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV core; 1.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15022 MW; A8F6C45366AA0B6E CRC64;

Query Match 91.5%; Score 43; DB 2; Length 137;
Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 99 DLMGYIPV 107

RESULT 10
Q5UBV2_9HEPC PRELIMINARY; PRT; 167 AA.
AC Q5UBV2;
DT 01-FEB-2005 (TRENBLrel. 29, Created)
DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=111103;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KNG318;
RA Chub E.V., Shustov A.V., Netesov S.V.;
RT "Intergenotypic recombinants of Hepatitis C virus found in Sough
RT Siberia.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY764170; AAV35986.1; -; Genomic_RNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV core.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV core; 1.
FT NON_TER 167 167
SQ SEQUENCE 167 AA; 18299 MW; D3296D178CD710FC CRC64;

Query Match 91.5%; Score 43; DB 2; Length 167;
Best Local Similarity 88.9%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 11
O09740_9HEPC PRELIMINARY; PRT; 188 AA.
AC O09740;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Nucleocapsid protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=111103;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RA Lerat H., Rumin S., Habersetzer F., Berby F., Traubaud M.-A., Trepo C.,
RA Inchauspe G.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBSJ databases.
RN [2]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93224886; PubMed=8385694;
RA Simmonds P., McOmish F., Yap P.L., Chan S.-W.W., Lin C.K.,
RA Dusheiko G., Saeed A.A., Holmes E.C.;
RT "Sequence variability in the 5' non-coding region of hepatitis C
RT virus: identification of a new virus type and restrictions on sequence
RT diversity.";
RL J. Gen. Virol. 74:661-668(1993).
DR EMBL; U94724; AA551539.1; -; Genomic_RNA.
DR FIR; P00804; P00804.
DR HSP; Q8JYS1; 1CW.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV core.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV core; 1.
KW Viral nucleoprotein.
FT NON_TER 188 188
SQ SEQUENCE 188 AA; 20597 MW; 22CFA884F136B44A CRC64;

Query Match 91.5%; Score 43; DB 2; Length 188;
Best Local Similarity 88.9%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

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RESULT 12
Q68411_9HEPC
ID Q68411_9HEPC PRELIMINARY; PRT; 191 AA.
AC Q68411;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus type 6.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=42182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97052554; PubMed=8897189;
RA Bernier L., Wilens B., Delage G., Murphy D.G.;
RT "Identification of numerous hepatitis C virus genotypes in Montreal,
Canada.";
RL J. Clin. Microbiol. 34:2815-2818(1996).
DR EMBL; U33435; AAB40038.1; -; Genomic_RNA.
DR HSP; Q8JYS1; ICWX.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
FT NON_TER 191
SQ SEQUENCE 191 AA; 20789 MW; F292AB64B56DE30A CRC64;

Query Match 91.5%; Score 43; DB 2; Length 191;
Best Local Similarity 88.9%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
DB 132 DLMGYIPV 140

RESULT 13
Q8BES0_9HEPC
ID Q8BES0_9HEPC PRELIMINARY; PRT; 191 AA.
AC Q8BES0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Core protein (Fragment).
GN Name=core;
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Serum;
RX MEDLINE=22913822; PubMed=1450584; DOI=10.1016/S0168-1702(03)00218-1;
RA Dansako H., Naganuma A., Nakamura T., Ikeda F., Nozaki A., Kato N.;
RT "Differential activation of interferon-inducible genes by hepatitis C
virus core protein mediated by the interferon stimulated response
element.";
RL Virus Res. 97:17-30(2003).
DR EMBL; AB029963; BAC20465.1; -; Genomic_RNA.
DR HSP; Q8JYS1; ICWX.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
FT NON_TER 191
SQ SEQUENCE 191 AA; 20765 MW; 97CE8EF4D13E479 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 191;

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Best Local Similarity 88.9%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
DB 132 DLMGYIPV 140

RESULT 14
Q8JW46_9HEPC
ID Q8JW46_9HEPC PRELIMINARY; PRT; 191 AA.
AC Q8JW46;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kato T., Wakita T.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB077951; BAC03374.1; -; mRNA.
DR HSP; Q8JYS1; ICWX.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
FT NON_TER 191
SQ SEQUENCE 191 AA; 20676 MW; E2EB9C99F5E08240 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 191;
Best Local Similarity 88.9%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
DB 132 DLMGYIPV 140

RESULT 15
Q68107_9HEPC
ID Q68107_9HEPC PRELIMINARY; PRT; 191 AA.
AC Q68107;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polypeptide (Fragment).
GN Name=C;
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DK11;
RX MEDLINE=94336721; PubMed=8058787;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the core gene of 14 hepatitis C virus
genotypes.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:8239-8243(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DK11;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
RN [3]

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Q68128_9HEPC
ID Q68128_9HEPC PRELIMINARY; PRT; 191 AA.
AC Q68128;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Polypeptide (Fragment).
GN Name=C;
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OC NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=S83;
RX MEDLINE=943336721; PubMed=8058787;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the core gene of 14 hepatitis C virus
genotypes."
RL Proc. Natl. Acad. Sci. U.S.A. 91:8239-8243(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=S83;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=S83;
RX MEDLINE=93376778; PubMed=8396266;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "At least 12 genotypes of hepatitis C virus predicted by sequence
RT analysis of the putative E1 gene of isolates collected worldwide."
RL Proc. Natl. Acad. Sci. U.S.A. 90:8234-8238(1993).
DR EMBL; U0211; AAA21050.1; -; Genomic_RNA.
DR HSP; Q8YSL1; ICWX.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR Polyprotein.
FT CHAIN 1 >191 core protein.
FT NON_TPR 191
SQ SEQUENCE 191 AA; 20749 MW; BB487813D174E221 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 191;
Best Local Similarity 88.9%; Pred. NO. 4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140
|||||||
|

RESULT 19
Q68141_9HEPC
ID Q68141_9HEPC PRELIMINARY; PRT; 191 AA.
AC Q68141;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Polypeptide (Fragment).
GN Name=C;
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OC NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SW3;

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RX MEDLINE=93376778; PubMed=8396266;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "At least 12 genotypes of hepatitis C virus predicted by sequence
RT analysis of the putative E1 gene of isolates collected worldwide.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:8234-8238(1993).
DR EMBL; U10226; AAA21065.1; -; Genomic_RNA.
DR HSSP; Q8JYS1; 1CWK.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
KW Polyprotein.
FT CHAIN 1 >191 core protein.
FT NON_TER 191
FT SEQUENCE 191 AA; 20761 MW; 882041ED38514CC1 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 191;
Best Local Similarity 88.9%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140
|||||

RESULT 21
Q68146_9HEPC
ID Q68146_9HEPC PRELIMINARY; PRT; 191 AA.
AC Q68146;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Polyprotein (Fragment).
DE Name=C;
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=T8;
RX MEDLINE=94336721; PubMed=8058787;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the core gene of 14 hepatitis C virus
RT genotypes.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:8239-8243(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=T8;
RX MEDLINE=94336721; PubMed=8058787;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=T8;
RX MEDLINE=94336721; PubMed=8058787;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the core gene of 14 hepatitis C virus
RT genotypes.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:8239-8243(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=T8;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=T8;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=T8;
RX MEDLINE=93376778; PubMed=8396266;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "At least 12 genotypes of hepatitis C virus predicted by sequence
RT analysis of the putative E1 gene of isolates collected worldwide.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:8234-8238(1993).
DR EMBL; U10229; AAA21068.1; -; Genomic_RNA.
DR HSSP; Q8JYS1; 1CWK.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
KW Polyprotein.
FT CHAIN 1 >191 core protein.
FT NON_TER 191
FT SEQUENCE 191 AA; 20710 MW; 35CB96B596C1B40D CRC64;

Query Match 91.5%; Score 43; DB 2; Length 191;
Best Local Similarity 88.9%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140
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RESULT 23
Q68148_9HEPC
ID Q68148_9HEPC PRELIMINARY; PRT; 191 AA.

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FT NON_TER 191
FT SEQUENCE 191 AA; 20815 MW; 33B563C1AD96E1AE CRC64;

Query Match 91.5%; Score 43; DB 2; Length 191;
Best Local Similarity 88.9%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140
|||||

RESULT 22
Q68147_9HEPC
ID Q68147_9HEPC PRELIMINARY; PRT; 191 AA.
AC Q68147;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Polyprotein (Fragment).
DE Name=C;
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=T9;
RX MEDLINE=94336721; PubMed=8058787;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the core gene of 14 hepatitis C virus
RT genotypes.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:8239-8243(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=T9;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=T9;
RX MEDLINE=93376778; PubMed=8396266;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "At least 12 genotypes of hepatitis C virus predicted by sequence
RT analysis of the putative E1 gene of isolates collected worldwide.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:8234-8238(1993).
DR EMBL; U10230; AAA21069.1; -; Genomic_RNA.
DR HSSP; Q8JYS1; 1CWK.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
KW Polyprotein.
FT CHAIN 1 >191 core protein.
FT NON_TER 191
FT SEQUENCE 191 AA; 20710 MW; 35CB96B596C1B40D CRC64;

Query Match 91.5%; Score 43; DB 2; Length 191;
Best Local Similarity 88.9%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140
|||||

RESULT 23
Q68148_9HEPC
ID Q68148_9HEPC PRELIMINARY; PRT; 191 AA.

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RA	Bukh J., Purcell R.H., Miller R.H.;
RT	"Sequence analysis of the core gene of 14 hepatitis C virus
RL	genotypes.";
RN	Proc. Natl. Acad. Sci. U.S.A. 91:8239-8243(1994).
RP	[2]
RC	NUCLEOTIDE SEQUENCE.
RD	STRAIN=US1;
RX	MEDLINE=92279243; PubMed=1317578;
RA	Bukh J., Purcell R.H., Miller R.H.;
RT	"Sequence analysis of the 5' noncoding region of hepatitis C virus."
RL	Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
RN	[3]
RP	NUCLEOTIDE SEQUENCE.
RD	STRAIN=US1;
RX	MEDLINE=93376778; PubMed=8396266;
RA	Bukh J., Purcell R.H., Miller R.H.;
RT	"At least 12 genotypes of hepatitis C virus predicted by sequence
RL	analysis of the putative E1 gene of isolates collected worldwide.";
RN	Proc. Natl. Acad. Sci. U.S.A. 90:8234-8238(1993).
DR	EMBL; U10233; AAA21072.1; -; Genomic_RNA.
DR	HSP; Q8JYS1; ICW.
DR	GO; GO:0019028; C:viral capsid; IEA.
DR	GO; GO:0005198; F:structural molecule activity; IEA.
DR	InterPro; IPR002522; HCV_capsid.
DR	InterPro; IPR002521; HCV_core.
DR	Pfam; PF01543; HCV_capsid; 1.
DR	Pfam; PF01542; HCV_core; 1.
KW	Polyprotein.
FT	CHAIN 1 >191
FT	NON_TER 191 191
FT	SEQUENCE 191 AA; 20711 MW; 1EAA41FCAD96F299 CRC64;
SQ	
	Query Match 91.5%; Score 43; DB 2; Length 191;
	Best Local Similarity 88.9%; Pred. No. 4;
	Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps
Qy	1 DLMGYIPAV 9
Db	
	132 DLMGYIPV 140
RESULT 25	
ID	Q68109_9HEPC PRELIMINARY; PRT; 191 AA.
AC	Q68109;
DT	01-NOV-1996 (TrEMBLrel. 01, Created)
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Polyprotein (Fragment).
GS	Name=C;
OS	Hepatitis C virus.
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC	Hepadnavirus.
OX	NCBI_taxid=i1103;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RD	STRAIN=DK13;
RX	MEDLINE=94336721; PubMed=8058787;
RA	Bukh J., Purcell R.H., Miller R.H.;
RT	"Sequence analysis of the core gene of 14 hepatitis C virus
RL	genotypes.";
RN	Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
RP	[2]
RC	NUCLEOTIDE SEQUENCE.
RD	STRAIN=DK13;
RX	MEDLINE=92279243; PubMed=1317578;
RA	Bukh J., Purcell R.H., Miller R.H.;
RT	"Sequence analysis of the 5' noncoding region of hepatitis C virus."
RL	Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
RN	[3]
RP	NUCLEOTIDE SEQUENCE.
RD	STRAIN=DK13;
RX	MEDLINE=93376778; PubMed=8396266;

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RA Bukh J., Purcell R.H., Miller R.H.;
RT "At least 12 genotypes of hepatitis C virus predicted by sequence
RL analysis of the putative E1 gene of isolates collected worldwide.";
RN Proc. Natl. Acad. Sci. U.S.A. 90:8234-8238(1993).
[4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93224886; PubMed=8385694;
RA Simmonds P., McMahon F., Yap P.L., Chan S.-W.W., Lin C.K.,
RA Dushenko G., Saeed A.A., Holmes E.C.;
RT "Sequence variability in the 5' non-coding region of hepatitis C
RT virus: identification of a new virus type and restrictions on sequence
RT diversity.";
RL J. Gen. Virol. 74:661-668(1993).
DR EMBL, U010192; AAA21031.1; -; Genomic_RNA.
DR FIR, PQ0804; PQ0804.
DR HSP, Q8JYS1; ICWX.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV core.
DR Pfam; PF01543; HCV capsid; 1.
DR Pfam; PF01542; HCV core; 1.
KW Polypeptide.
FT CHAIN 1 >191 core protein.
FT NON_TER 191
SQ SEQUENCE 191 AA; 20770 MW; D0D9700694886D87 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 191;
Best Local Similarity 88.9%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
DB 132 DLMGYIPV 140

RESULT 26
Q68711_9HEPC
ID Q68711_9HEPC PRELIMINARY; PRT; 192 AA.
AC Q68711;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Core protein (fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=CH114 genotype 2c;
RX MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;
RA Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P.,
RA Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,
RA Maertens G.;
RT "Hepatitis C virus genotyping by means of 5'-UR/core line probe assays
RT and molecular analysis of untypeable samples.";
RL Virus Res. 38:137-157(1995).
DR EMBL, L38257; AAC42207.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002521; HCV core.
DR InterPro; IPR002519; HCV env.
DR Pfam; PF01542; HCV core; 1.
DR Pfam; PF01539; HCV env; 1.
KW Envelope protein; Polypeptide; Transmembrane.
FT CHAIN <1 65 core protein.
FT CHAIN 66 >192 E1 protein.
FT NON_TER 1 1
FT NON_TER 192 192
SQ SEQUENCE 192 AA; 20272 MW; 65CDS479AF99938 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 193;
Best Local Similarity 88.9%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
DB 6 DLMGYIPV 14

RESULT 28
Q81558_9HEPC
ID Q81558_9HEPC PRELIMINARY; PRT; 193 AA.
AC Q81558;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE (NE92) core protein (fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=NE92;
RX MEDLINE=95023999; PubMed=7524083;
RA Stuyver L., van Arnhem W., Wyseur A., Hernandez F., Delaporte E.,
RA Maertens G.;

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Query Match 91.5%; Score 43; DB 2; Length 192;
Best Local Similarity 88.9%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
DB 6 DLMGYIPV 14

RESULT 27
Q68709_9HEPC
ID Q68709_9HEPC PRELIMINARY; PRT; 193 AA.
AC Q68709;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Polypeptide (fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=BE104 genotype 2c;
RX MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;
RA Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P.,
RA Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,
RA Maertens G.;
RT "Hepatitis C virus genotyping by means of 5'-UR/core line probe assays
RT and molecular analysis of untypeable samples.";
RL Virus Res. 38:137-157(1995).
DR EMBL, L38257; AAC42208.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002521; HCV core.
DR InterPro; IPR002519; HCV env.
DR Pfam; PF01542; HCV core; 1.
DR Pfam; PF01539; HCV env; 1.
KW Envelope protein; Polypeptide; Transmembrane.
FT CHAIN <1 65 core protein.
FT CHAIN 66 >193 E1 protein.
FT NON_TER 1 1
FT NON_TER 193 193
SQ SEQUENCE 193 AA; 20272 MW; 65CDS479AF99938 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 193;
Best Local Similarity 88.9%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
DB 6 DLMGYIPV 14

RESULT 28
Q81558_9HEPC
ID Q81558_9HEPC PRELIMINARY; PRT; 193 AA.
AC Q81558;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE (NE92) core protein (fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=NE92;
RX MEDLINE=95023999; PubMed=7524083;
RA Stuyver L., van Arnhem W., Wyseur A., Hernandez F., Delaporte E.,
RA Maertens G.;

```


RT "Classification of hepatitis C viruses based on phylogenetic analysis of the envelope 1 and nonstructural 5B regions and identification of five additional subtypes.";

RL Proc. Natl. Acad. Sci. U.S.A. 91:10134-10138(1994).

DR EMBL; L29633; AAA65816.1; -; Genomic_RNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR002521; HCV_Core.

DR InterPro; IPR002519; HCV_env.

DR Pfam; PF01542; HCV_core; 1.

DR Pfam; PF01539; HCV_env; 1.

KW Envelope protein; Transmembrane.

FT CHAIN <1 65 core protein.

FT CHAIN 66 >193 envelope protein.

FT NON_TER 1 1

FT NON_TER 193 193

SQ SEQUENCE 193 AA; 20460 MW; 04BEAA5213688270 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 193;

Best Local Similarity 88.9%; Pred. NO. 4.1;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9

|||||

Db 6 DLMGYIPV 14

RESULT 29

Q91TF6_9HEPC

ID Q91TF6_9HEPC PRELIMINARY; PRT; 195 AA.

AC Q91TF6_

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Polyprotein (Fragment).

OS Hepatitis C virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Hepacivirus.

OX NCBI_TaxID=11103;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=AR46;

RX MEDLINE=21225609; PubMed=11326031;

RX DOI=10.1126/JCW.33.5.1989-1992.2001;

RA Alfonso V., Flichman D., Sookoian S., Mbayed V.A., Campos R.H.;

"Phylogenetic characterization of genotype 4 hepatitis C virus

isolates from Argentina.";

RL J. Clin. Microbiol. 39:1989-1992(2001).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=93224886; PubMed=8385694;

RA Simmonds P., McOmish F., Yap P.L., Chan S.-W.W., Lin C.K.,

Dusheiko G., Saeed A.A., Holmes E.C.;

"Sequence variability in the 5' non-coding region of hepatitis C

virus: identification of a new virus type and restrictions on sequence

diversity.";

RL J. Gen. Virol. 74:661-668(1993).

DR EMBL; AF308577; AAK54689.1; -; Genomic_RNA.

DR PIR; PQ0804; PQ0804.

DR HSP; Q8JYS1; 1CW.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR002522; HCV_capsid.

DR InterPro; IPR002521; HCV_core.

DR Pfam; PF01543; HCV_capsid; 1.

DR Pfam; PF01542; HCV_core; 1.

KW Polyprotein.

FT CHAIN 1 >195 core protein.

FT NON_TER 195 195

SQ SEQUENCE 195 AA; 21287 MW; 6608922F1F416577 CRC64;

Query Match

91.5%; Score 43; DB 2; Length 195;

Best Local Similarity 88.9%; Pred. NO. 4.1;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9

|||||

Db 132 DLMGYIPV 140

RESULT 30

Q68692_9HEPC

ID Q68692_9HEPC PRELIMINARY; PRT; 235 AA.

AC Q68692_

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Core protein (Fragment).

OS Hepatitis C virus type 2c.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Hepacivirus.

OX NCBI_TaxID=31651;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;

RA Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P.,

Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,

Maertens G.;

"Hepatitis C virus genotyping by means of 5'-UR/core line probe assays

and molecular analysis of untypeable samples.";

RL Virus Res. 38:137-157(1995).

DR EMBL; L38325; AAC42180.1; -; mRNA.

DR HSP; Q8JYS1; 1CW.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR002522; HCV_capsid.

DR InterPro; IPR002521; HCV_core.

DR Pfam; PF01543; HCV_capsid; 1.

DR Pfam; PF01542; HCV_core; 1.

DR Pfam; PF01539; HCV_env; 1.

KW Envelope protein; Transmembrane.

FT CHAIN 1 191 core protein.

FT NON_TER 192 >235 EI protein.

FT NON_TER 235 235

SQ SEQUENCE 235 AA; 25574 MW; C071BA485738856D CRC64;

Query Match 91.5%; Score 43; DB 2; Length 235;

Best Local Similarity 88.9%; Pred. NO. 4.9;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9

|||||

Db 132 DLMGYIPV 140

RESULT 31

Q68694_9HEPC

ID Q68694_9HEPC PRELIMINARY; PRT; 235 AA.

AC Q68694_

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Core protein (Fragment).

OS Hepatitis C virus type 2c.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Hepacivirus.

OX NCBI_TaxID=31651;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;

RA Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P.,

Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,

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RA Maertens G.;
RT "Hepatitis C virus genotyping by means of 5'-UR/core line probe assays
RT and molecular analysis of untypeable samples.";
RL Virus Res. 38:137-157(1995).
DR EMBL; L38327; AAC42182.1; -; mRNA.
DR HSSP; Q8JYS1; 1CWK.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV env.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR Pfam; PF01539; HCV_env; 1.
KW Envelope protein; Transmembrane.
FT CHAIN 1 191 core protein.
FT CHAIN 192 >313 E1 protein.
FT NON_TER 235 235
SQ SEQUENCE 235 AA; 25406 MW; D78FD1967FA18003 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 235;
Best Local Similarity 88.9%; Pred. No. 4.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 32
Q8687_9HEPC
ID Q68687_9HEPC PRELIMINARY; PRT; 313 AA.
AC Q68687;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus type 2c.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=31651;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;
RA Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P.,
RA Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,
RA Maertens G.;
RT "Hepatitis C virus genotyping by means of 5'-UR/core line probe assays
RT and molecular analysis of untypeable samples.";
RL Virus Res. 38:137-157(1995).
DR EMBL; L38322; AAC42177.1; -; mRNA.
DR HSSP; Q8JYS1; 1CWK.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV env.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR Pfam; PF01539; HCV_env; 1.
KW Envelope protein; Transmembrane.
FT CHAIN 1 191 core protein.
FT CHAIN 192 >317 E1 protein.
FT NON_TER 317 317
SQ SEQUENCE 317 AA; 34135 MW; 5EA77FFFD0239D31 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 317;
Best Local Similarity 88.9%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 34
Q8696_9HEPC
ID Q68696_9HEPC PRELIMINARY; PRT; 317 AA.
AC Q68696;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus type 2c.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=31651;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;
RA Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P.,
RA Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,
RA Maertens G.;
RT "Hepatitis C virus genotyping by means of 5'-UR/core line probe assays
RT and molecular analysis of untypeable samples.";
RL Virus Res. 38:137-157(1995).
DR EMBL; L38320; AAC42175.1; -; mRNA.
DR HSSP; Q8JYS1; 1CWK.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV env.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR Pfam; PF01539; HCV_env; 1.
KW Envelope protein; Transmembrane.
FT CHAIN 1 191 core protein.
FT CHAIN 192 >313 E1 protein.
FT NON_TER 313 313
SQ SEQUENCE 313 AA; 6548ABAE13932741 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 313;
Best Local Similarity 88.9%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 33
Q8689_9HEPC
ID Q68689_9HEPC PRELIMINARY; PRT; 317 AA.
AC Q68689;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus type 2c.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=31651;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;
RA Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P.,
RA Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,
RA Maertens G.;
RT "Hepatitis C virus genotyping by means of 5'-UR/core line probe assays
RT and molecular analysis of untypeable samples.";
RL Virus Res. 38:137-157(1995).
DR EMBL; L38322; AAC42177.1; -; mRNA.
DR HSSP; Q8JYS1; 1CWK.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV env.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR Pfam; PF01539; HCV_env; 1.
KW Envelope protein; Transmembrane.
FT CHAIN 1 191 core protein.
FT CHAIN 192 >317 E1 protein.
FT NON_TER 317 317
SQ SEQUENCE 317 AA; 34135 MW; 5EA77FFFD0239D31 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 317;
Best Local Similarity 88.9%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 34
Q8696_9HEPC
ID Q68696_9HEPC PRELIMINARY; PRT; 317 AA.
AC Q68696;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Core protein (Fragment).
OS Hepatitis C virus type 2c.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=31651;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;
RA Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P.,
RA Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,
RA Maertens G.;
RT "Hepatitis C virus genotyping by means of 5'-UR/core line probe assays
RT and molecular analysis of untypeable samples.";

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RT and molecular analysis of untypeable samples.;"

RL Virus Res. 38:137-157(1995).
 DR EMBL; L38329; AAC42184.1; -; mRNA.
 DR HSSP; Q8JYS1; 1CWX.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; F:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002522; HCV_capsid.
 DR InterPro; IPR002521; HCV_core.
 DR InterPro; IPR002519; HCV_env.
 DR Pfam; PF01543; HCV_capsid; 1.
 DR Pfam; PF01542; HCV_core; 1.
 DR Pfam; PF01539; HCV_env; 1.
 KW Envelope protein; Transmembrane.
 FT CHAIN 1 191 core protein.
 FT CHAIN 192 >317 E1 protein.
 FT NON_TER 317 317
 SQ SEQUENCE 317 AA; 34124 MW; C3AFE2297A4A16EC CRC64;

Query Match 91.5%; Score 43; DB 2; Length 317;
 Best Local Similarity 88.9%; Pred. No. 6.5;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 |||||
 Db 132 DLMGYIPV 140

RESULT 35
 Q6T663_9HEPC PRELIMINARY; PRT; 317 AA.
 AC Q6T663;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Polypeptide (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=QC66;
 RA Murphy D., Willems B., Deschenes M., Hilzenrat N., Mousseau R.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY34111; AAR12079.1; -; Genomic RNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002522; HCV_capsid.
 DR InterPro; IPR002521; HCV_core.
 DR InterPro; IPR002519; HCV_env.
 DR Pfam; PF01543; HCV_capsid; 1.
 DR Pfam; PF01542; HCV_core; 1.
 DR Pfam; PF01539; HCV_env; 1.
 KW Envelope protein; Polypeptide; Transmembrane.
 FT NON_TER 317 317
 SQ SEQUENCE 317 AA; 34062 MW; 1A3C3B818AD4FEC7 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 317;
 Best Local Similarity 88.9%; Pred. No. 6.5;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 |||||
 Db 132 DLMGYIPV 140

RESULT 36
 Q68691_9HEPC PRELIMINARY; PRT; 318 AA.
 ID Q68691_9HEPC PRELIMINARY;

AC Q68691;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Core protein (Fragment).
 OS Hepatitis C virus type 2c.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=31651;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;
 RA Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P.,
 RA Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,
 RA Maertens G.;
 RT "Hepatitis C virus genotyping by means of 5'-UR/core line probe assays
 RT and molecular analysis of untypeable samples.";
 RL Virus Res. 38:137-157(1995).
 DR EMBL; L38324; AAC42179.1; -; mRNA.
 DR HSSP; Q8JYS1; 1CWX.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002522; HCV_capsid.
 DR InterPro; IPR002521; HCV_core.
 DR InterPro; IPR002519; HCV_env.
 DR Pfam; PF01543; HCV_capsid; 1.
 DR Pfam; PF01542; HCV_core; 1.
 DR Pfam; PF01539; HCV_env; 1.
 KW Envelope protein; Transmembrane.
 FT CHAIN 1 191 core protein.
 FT CHAIN 192 >318 E1 protein.
 FT NON_TER 318 318
 SQ SEQUENCE 318 AA; 34463 MW; E7A5F7DE5B6A34FC CRC64;
 Query Match 91.5%; Score 43; DB 2; Length 318;
 Best Local Similarity 88.9%; Pred. No. 6.5;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 |||||
 Db 132 DLMGYIPV 140

RESULT 37
 Q81262_9HEPC PRELIMINARY; PRT; 318 AA.
 ID Q81262_9HEPC PRELIMINARY;
 AC Q81262;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Core protein (Fragment).
 OS Hepatitis C virus type 4f.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=44023;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;
 RA Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P.,
 RA Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,
 RA Maertens G.;
 RT "Hepatitis C virus genotyping by means of 5'-UR/core line probe assays
 RT and molecular analysis of untypeable samples.";
 RL Virus Res. 38:137-157(1995).
 DR EMBL; L38333; AAC42188.1; -; mRNA.
 DR HSSP; Q8JYS1; 1CWX.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002522; HCV_capsid.

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DR InterPro; IPR002521; HCV_core.
DR InterPro; IPR002519; HCV_env.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR Pfam; PF01539; HCV_env; 1.
DR Envelope protein; Transmembrane.
FT CHAIN 1 191 core protein.
FT NON_TER 192 318 El protein.
SQ SEQUENCE 318 AA; 34584 MW; 5D3F7649C3C20F1F CRC64;

Query Match 91.5%; Score 43; DB 2; Length 318;
Best Local Similarity 88.9%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 38
Q68678_9HEPC
ID Q68678_9HEPC PRELIMINARY; PRT; 319 AA.
AC Q68678;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Core protein (fragment).
OS Hepatitis C virus type 2c.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
NCBI_TaxID=31651;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;
RA Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P.,
RA Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,
RA Maertens G.;
RT "Hepatitis C virus genotyping by means of 5'-UR/core line probe assays
and molecular analysis of untypeable samples.";
RL Virus Res. 38:137-157(1995).
DR EMBL; L38319; AAC42164.1; -; mRNA.
DR HSSP; Q8JYS1; 1CWK.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR Pfam; PF01539; HCV_env; 1.
DR Envelope protein; Transmembrane.
FT CHAIN 1 191 core protein.
FT NON_TER 192 319 El protein.
SQ SEQUENCE 319 AA; 34503 MW; 222569EA0ACF43C CRC64;

Query Match 91.5%; Score 43; DB 2; Length 319;
Best Local Similarity 88.9%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 40
Q68693_9HEPC
ID Q68693_9HEPC PRELIMINARY; PRT; 319 AA.
AC Q68693;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Core protein (fragment).
OS Hepatitis C virus type 2c.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
NCBI_TaxID=31651;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;
RA Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P.,
RA Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,
RA Maertens G.;
RT "Hepatitis C virus genotyping by means of 5'-UR/core line probe assays
and molecular analysis of untypeable samples.";
RL Virus Res. 38:137-157(1995).
DR EMBL; L38326; AAC42181.1; -; mRNA.
DR HSSP; Q8JYS1; 1CWK.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR Envelope protein; Transmembrane.
FT CHAIN 1 191 core protein.
FT NON_TER 192 319 El protein.
SQ SEQUENCE 319 AA; 34534 MW; 6F2BE1167A9A9E7 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 319;
Best Local Similarity 88.9%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 39
Q68688_9HEPC
ID Q68688_9HEPC PRELIMINARY; PRT; 319 AA.
AC Q68688;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

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DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Core protein (fragment).
OS Hepatitis C virus type 2c.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
NCBI_TaxID=31651;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;
RA Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P.,
RA Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,
RA Maertens G.;
RT "Hepatitis C virus genotyping by means of 5'-UR/core line probe assays
and molecular analysis of untypeable samples.";
RL Virus Res. 38:137-157(1995).
DR EMBL; L38321; AAC42176.1; -; mRNA.
DR HSSP; Q8JYS1; 1CWK.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV_core.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR Pfam; PF01539; HCV_env; 1.
DR Envelope protein; Transmembrane.
FT CHAIN 1 191 core protein.
FT NON_TER 192 319 El protein.
SQ SEQUENCE 319 AA; 34503 MW; 222569EA0ACF43C CRC64;

Query Match 91.5%; Score 43; DB 2; Length 319;
Best Local Similarity 88.9%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 40
Q68693_9HEPC
ID Q68693_9HEPC PRELIMINARY; PRT; 319 AA.
AC Q68693;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Core protein (fragment).
OS Hepatitis C virus type 2c.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
NCBI_TaxID=31651;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=96118171; PubMed=8578855; DOI=10.1016/0168-1702(95)00052-R;
RA Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P.,
RA Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J.,
RA Maertens G.;
RT "Hepatitis C virus genotyping by means of 5'-UR/core line probe assays
and molecular analysis of untypeable samples.";
RL Virus Res. 38:137-157(1995).
DR EMBL; L38326; AAC42181.1; -; mRNA.
DR HSSP; Q8JYS1; 1CWK.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV_core.

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DR Pfam; PF01543; HCV_capsid; 1.
 DR Pfam; PF01542; HCV_core; 1.
 DR Pfam; PF01539; HCV_env; 1.
 KW Envelope protein; Transmembrane.
 FT CHAIN 1 191 core protein.
 FT CHAIN 192 >319 E1 protein.
 FT NON_TER 319 319
 SQ SEQUENCE 319 AA; 34268 MW; 6357221F0F1E5899 CRC64;
 Query Match 91.5%; Score 43; DB 2; Length 319;
 Best Local Similarity 88.9%; Pred. No. 6.5;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DLMGYIPAV 9
 Db 132 DLMGYIPV 140

Search completed: January 20, 2006, 22:41:33
 Job time : 72 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 20, 2006, 22:29:13 ; Search time 16 Seconds

(without alignments)

54.122 Million cell updates/sec

Title: US-10-770-117-1

Perfect score: 47

Sequence: 1 DLMGYIPAV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 80:*

1: Pirl:*

2: Pirl:*

3: Pirl:*

4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	91.5	874	2 JQ0883	genome polyprotein
2	43	91.5	874	2 JQ0881	genome polyprotein
3	43	91.5	3033	1 GNMVJ8	genome polyprotein
4	43	91.5	3033	1 JQ1303	genome polyprotein
5	42	89.4	178	2 PS0388	genome polyprotein
6	42	89.4	189	2 S32740	polyprotein - hepa
7	42	89.4	322	2 JN0265	genome polyprotein
8	42	89.4	369	2 S21471	genome polyprotein
9	42	89.4	411	2 PC2061	genome polyprotein
10	42	89.4	411	2 PC2060	genome polyprotein
11	42	89.4	441	2 S12707	genome polyprotein
12	42	89.4	492	2 PC1288	genome polyprotein
13	42	89.4	513	2 PC1284	genome polyprotein
14	42	89.4	513	2 A44150	structural protein
15	42	89.4	520	2 JQ1925	polyprotein - hepa
16	42	89.4	523	2 JQ1926	polyprotein - hepa
17	42	89.4	550	2 JH0711	genome polyprotein
18	42	89.4	640	2 JQ1584	genome polyprotein
19	42	89.4	782	2 S18032	genome polyprotein
20	42	89.4	782	2 S18031	genome polyprotein
21	42	89.4	782	2 S19875	genome polyprotein
22	42	89.4	787	2 PN0677	hypothetical prote
23	42	89.4	876	2 PC2219	polypeptide - hepa
24	42	89.4	3010	1 A45573	genome polyprotein
25	42	89.4	3010	1 GNMVJ3	genome polyprotein
26	42	89.4	3010	1 GNMVTC	genome polyprotein
27	42	89.4	3010	1 GNMVTV	genome polyprotein
28	42	89.4	3010	1 S18030	genome polyprotein
29	42	89.4	3011	1 GNMVJ3	genome polyprotein

genome polyprotein
genome polyprotein
phospho-beta-galac
betaine aldehyde d
genome polyprotein
precorrin-3 methyl
hypothetical prote
formate dehydrogen
DNA topoisomerase
topoisomerase IV c
genome polyprotein
dmp-4-keto-6-deox
probable precorrin
6-phospho-beta-glu
6-phospho-beta-glu
beta-glucosidase (
phospho-beta-gluco
6-phospho-beta-glu
bglA protein - Esc
6-phospho-beta-glu
6-phospho-beta-glu
probable propionyl
hypoxia-inducible
conserved hypotet
stress induced hyd
allergen Mal f2 -
endopeptidase Clp
transglycosylase h
rod shape-determin
conserved hypotet
conserved hypotet
histidinol dehydro
citrate carrier pr
citrate-sodium sym
citrate carrier pr
citrate transport
H+-transporting tw
chaperonin 60 alph
hypothetical prote
hypothetical prote
major single-stran
tubulin-folding co
ribulose-bisphosph
ribulose 1,5-bisph
ribulose-bisphosph
NADP-reducing hydr
hypothetical prote
hypothetical prote
Probable inner-mem
hypothetical prote
beta-fructofuranos
TDP-glucose-4,6-de
cobalamin biosynth
hypothetical prote
GTPase activating
hypothetical prote
L-serine dehydrata
hypothetical prote
hypothetical prote
probable glucosylt
coccylasin (EC 3.4
Eas9 protein - pha
ABC transporter, A
hypothetical prote
nucleoside diphosp
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hypothetical prote
hypothetical prote

ALIGNMENTS

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RESULT 1
genome polyprotein - hepatitis C virus (strain J7) (fragments)
N:Contains: NS5 protein
C:Species: hepatitis C virus
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: JQ0883
R:Okamoto, H.
submitted to JIPID, January 1991
A:Description: The 5'-terminal and 3'-terminal sequences of the genomic RNA of hepatitis
A:Reference number: JQ0879
A:Accession: JQ0883
A:Molecule type: genomic RNA
A:Residues: 1-874 <OKA>
A:Cross-references: UNIPROT:Q7LZY6; UNIPARC:UPI0000178537
A:Experimental source: strain J7
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: polyprotein
F:510-874/Product: NS5 protein (fragment) #status predicted <NS5>

Query Match          91.5%; Score 43; DB 2; Length 874;
Best Local Similarity 88.9%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
    |||||
Db 132 DLMGYIPV 140

RESULT 2
genome polyprotein - hepatitis C virus (strain J6) (fragments)
N:Contains: NS5 protein
C:Species: hepatitis C virus
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: JQ0881
R:Okamoto, H.
submitted to JIPID, January 1991
A:Description: The 5'-terminal and 3'-terminal sequences of the genomic RNA of hepatitis
A:Reference number: JQ0879
A:Accession: JQ0881
A:Molecule type: genomic RNA
A:Residues: 1-874 <OKA>
A:Cross-references: UNIPROT:Q7LZY5; UNIPARC:UPI0000178538
A:Experimental source: strain J6
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: polyprotein
F:510-874/Product: NS5 protein (fragment) #status predicted <NS5>

Query Match          91.5%; Score 43; DB 2; Length 874;
Best Local Similarity 88.9%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
    |||||
Db 132 DLMGYIPV 140

RESULT 3
genome polyprotein - hepatitis C virus (strain HC-J8)
N:Contains: capsid protein C; envelope protein M; hepatitis C virus (nonstructural
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C:Species: hepatitis C virus
C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C:Accession: A40250; P00397; P00559
R:Okamoto, H.; Kurai, K.; Okada, S.I.; Yamamoto, K.; Lizuka, H.; Tanaka, T.; Fukuda, S.;
Virology 188, 331-341, 1992
A:Title: Full-length sequence of a hepatitis C virus genome having poor homology to rep
A:Reference number: A40250; MUID:92230232; PMID:1314459
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A:Accession: A40250
A:Molecule type: genomic RNA
A:Residues: 1-3033 <OKA>
A:Cross-references: UNIPROT:P26661; UNIPARC:UPI0000131E27; GB:D10988; GB:D01221; NID:9
R:Chan, S.W.; McOmish, F.; Holmes, E.C.; Dow, B.; Peutherer, J.F.; Follett, E.; Yap, P
J. Gen. Virol. 73, 1131-1141, 1992
A:Title: Analysis of a new hepatitis C virus type and its phylogenetic relationship to
A:Reference number: P00393; MUID:92268871; PMID:1316939
A:Accession: P00397
A:Molecule type: genomic RNA
A:Residues: 2678-2754 <CHA>
A:Cross-references: UNIPARC:UPI0000174A02; DDBJ:D10134
A:Experimental source: isolate E-bi2
R:Kato, N.; Ootsuyama, Y.; Ohkoshi, S.; Nakazawa, T.; Mori, S.; Hijikata, M.; Shimotoh
Biochem. Biophys. Res. Commun. 181, 279-285, 1991
A:Title: Distribution of plural HCV types in Japan.
A:Reference number: P00554; MUID:92068204; PMID:1720309
A:Accession: P00559
A:Molecule type: mRNA
A:Residues: 2678-2729 <KAT>
A:Cross-references: UNIPARC:UPI00000F5263; GB:D10562; GB:D90518; NID:G221523; PIDN:BAA
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructu
F:115-191/Product: capsid protein C #status predicted <CPC>
F:192-389/Product: envelope protein M #status predicted <EPM>
F:730-733/Product: major envelope protein NS1 #status predicted <NS1>
F:734-1010/Product: nonstructural protein NS2 #status predicted <NS2>
F:1011-1619/Product: hepatitis C virus #status predicted <NS3>
F:1234-1241/Region: nucleotide-binding motif A (P-loop)
F:1316-1321/Region: nucleotide-binding motif B
F:1320-1323/Region: DEXH motif
F:1620-1866/Product: nonstructural protein NS4a #status predicted <NS4>
F:1867-2017/Product: nonstructural protein NS4b #status predicted <NS4>
F:2018-3033/Product: nonstructural protein NS5 #status predicted <NS5>
F:196,209,233,299,305,417,423,430,448,477,534,542,558,578,627,649,1091,1217,1259,2038,

Query Match          91.5%; Score 43; DB 1; Length 3033;
Best Local Similarity 88.9%; Pred. No. 7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
    |||||
Db 132 DLMGYIPV 140

RESULT 4
genome polyprotein - hepatitis C virus (isolate HC-J6)
N:Contains: capsid protein C; envelope protein M; hepatitis C virus (nonstructural
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C:Species: hepatitis C virus
C>Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: JQ1303
R:Okamoto, H.; Okada, S.; Sugiyama, Y.; Kurai, K.; Iizuka, H.; Machida, A.; Miyakawa,
J. Gen. Virol. 72, 2697-2704, 1991
A:Title: Nucleotide sequence of the genomic RNA of hepatitis C virus isolated from a h
A:Reference number: JQ1303; MUID:92044440; PMID:1658196
A:Accession: JQ1303
A:Molecule type: genomic RNA
A:Residues: 1-3033 <OKA>
A:Cross-references: UNIPROT:P26660; UNIPARC:UPI0000131E25; GB:D00944; NID:G221650; PID
A:Experimental source: isolate HC-J6 from a Japanese individual
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: ATP; glycoprotein; hydrolase; P-loop; polyprotein; serine proteinase; tran
F:2-115/Product: capsid protein C #status predicted <CPC>
F:116-191/Product: envelope protein M #status predicted <EPM>
F:192-389/Product: major envelope protein E #status predicted <MEB>
F:730-733/Product: nonstructural protein NS1 #status predicted <NS1>
F:734-1010/Product: nonstructural protein NS2 #status predicted <NS2>
F:1011-1619/Product: hepatitis C virus #status predicted <NS3>
F:1316-1321/Region: nucleotide-binding motif B
F:1320-1323/Region: DEXH motif
```

F:1620-1866/Product: nonstructural protein NS4a #status predicted <N4A>
 F:1867-2017/Product: nonstructural protein NS4b #status predicted <N4B>
 F:2018-3033/Product: nonstructural protein NS5 #status predicted <NOS>
 F:196,209,234,305,325,417,423,430,448,477,534,542,558,578,627,649,1091,1217,1259,2038,28

Query Match 91.5%; Score 43; DB 1; Length 3033;
 Best Local Similarity 88.9%; Pred. No. 7;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 |||||
 DB 132 DLMGYIPV 140

RESULT 5
 PS0388
 genome polyprotein - hepatitis C virus (isolate GM1) (fragment)
 N:Contains: amino end of envelope protein M; carboxyl end of capsid protein C
 C:Species: hepatitis C virus
 A:Note: host Homo sapiens (man)
 C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
 C:Accession: PS0388
 R:Fuchs, K.; Motz, M.; Schreier, E.; Zachoval, R.; Roggendorf, M.
 Gene 103, 163-169, 1991
 A:Title: Characterization of nucleotide sequences from European hepatitis C virus isolat
 A:Reference number: JN0265; MUID:91365241; PMID:1653756
 A:Accession: PS0388
 A:Molecule type: genomic RNA
 A:Residues: 1-178 <FUC>
 A:CROSS-references: UNIPROT:O81275; UNIPARC:UPI0000F0A6E; GB:M61719; NID:G329757; PIDN:
 C:Superfamily: hepatitis C virus genome polyprotein
 C:Keywords: capsid protein; envelope protein; polyprotein; transmembrane protein
 F:1-109/Product: capsid protein C (fragment) #status predicted <CPC>
 F:110-178/Product: envelope protein M (fragment) #status predicted <BPM>
 F:163-178/Domain: transmembrane #status predicted <TM1>

Query Match 89.4%; Score 42; DB 2; Length 178;
 Best Local Similarity 88.9%; Pred. No. 0.61;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 |||||
 DB 126 DLMGYIPV 134

RESULT 6
 S32740
 polyprotein - hepatitis C virus (isolate Russian) (fragment)
 N:Contains: capsid protein C; envelope protein M
 C:Species: hepatitis C virus
 C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
 C:Accession: S32740
 R:Vassilev, V.B.; Viazov, S.O.; Kotova, E.Y.; Nosikov, V.V.
 submitted to the EMBL Data Library, April 1993
 A:Description: Evidence of new HCV variant of European isolate in Russia.
 A:Reference number: S32740
 A:Accession: S32740
 A:Molecule type: genomic RNA
 A:Residues: 1-189 <VAS>
 A:CROSS-references: UNIPROT:Q68873; UNIPARC:UPI0000178544; EMBL:X71407
 C:Superfamily: hepatitis C virus genome polyprotein
 C:Keywords: capsid protein; envelope protein; polyprotein
 F:1-115/Product: capsid protein C #status predicted <CPC>
 F:116-189/Product: envelope protein M #status predicted <BPM>

Query Match 89.4%; Score 42; DB 2; Length 189;
 Best Local Similarity 88.9%; Pred. No. 0.65;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 |||||
 DB 132 DLMGYIPV 140

RESULT 7

JN0265
 genome polyprotein - hepatitis C virus (isolate GM2) (fragments)
 N:Contains: amino end of envelope protein M; carboxyl end of capsid protein C; fragmen
 C:Species: hepatitis C virus
 A:Note: host Homo sapiens (man)
 C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 31-Dec-2004
 C:Accession: JN0265
 R:Fuchs, K.; Motz, M.; Schreier, E.; Zachoval, R.; Deinhardt, F.; Roggendorf, M.
 Gene 103, 163-169, 1991
 A:Title: Characterization of nucleotide sequences from European hepatitis C virus isol
 A:Reference number: JN0265; MUID:91365241; PMID:1653756
 A:Accession: JN0265
 A:Molecule type: genomic RNA
 A:Residues: 1-322 <FUC>
 A:CROSS-references: UNIPROT:Q03729; UNIPARC:UPI00001784F5; GB:M61717; GB:M61718
 A:Note: the authors translated the codon ACA for residue 198 as Tyr
 C:Keywords: capsid protein; envelope protein; glycoprotein; polyprotein; transmembrane
 F:1-109/Product: capsid protein C (fragment) #status predicted <COR>
 F:110-178/Product: envelope protein M (fragment) #status predicted <BPM>
 F:163-178/Domain: transmembrane #status predicted <TM1>
 F:179-322/Product: major envelope protein E (fragment) #status predicted <ENV>
 F:253-269/Domain: transmembrane #status predicted <TM2>
 F:191,216/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.4%; Score 42; DB 2; Length 322;

Best Local Similarity 88.9%; Pred. No. 1.1;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9

|||||

DB 126 DLMGYIPV 134

RESULT 8

S21471
 genome polyprotein - hepatitis C virus (fragment)
 N:Contains: capsid protein; envelope protein

C:Species: hepatitis C virus

C:Date: 20-Feb-1995 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C:Accession: S21471

R:Mogam, W.K.

submitted to the EMBL Data Library, April 1992

A:Reference number: S21471

A:Accession: S21471

A:Molecule type: genomic RNA

A:Residues: 1-369 <MOG>

A:CROSS-references: UNIPROT:Q68869; UNIPARC:UPI00000F3A9C; EMBL:X65924; NID:G59466; PI

C:Superfamily: hepatitis C virus genome polyprotein

C:Keywords: capsid protein; envelope protein; glycoprotein; polyprotein

Query Match

89.4%; Score 42; DB 2; Length 369;

Best Local Similarity 88.9%; Pred. No. 1.3;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9

|||||

DB 132 DLMGYIPV 140

RESULT 9

PC2061
 genome polyprotein N2 - hepatitis C virus

N:Contains: envelope protein E1; nonstructural protein E2/NS1

C:Species: hepatitis C virus

C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004

C:Accession: PC2061

R:Li, J.S.; Vitvitski, L.; Tong, S.P.; Trepo, C.

Biochem. Biophys. Res. Commun. 199, 1474-1481, 1994

A:Title: Identification of the third major genotype of hepatitis C virus in France.

A:Reference number: PC2060; MUID:94197744; PMID:8147893

A:Accession: PC2061


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A:Molecule type: mRNA
A:Residues: 1-411 <LIJ>
A:Cross-references: UNIPROT:Q81813; UNIPARC:UPI00000F900B; GB:L12355; NID:G410169; PIDN:
S41288
C:Superfamily: hepatitis C virus genome polyprotein
N/Contains: core protein; envelope protein; glycoprotein; nonstructural protein;
C/Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;
F:192-383/Product: envelope protein E1 #status predicted <SPE>
F:384-411/Product: nonstructural protein E2/NS1 #status predicted <NPE>
F:196,209,234,305,325/Binding site: carbonylate (Asn) (covalent) #status predicted

Query Match      89.4%; Score 42; DB 2; Length 411;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
      |||||
Db      132 DLMGYIPLV 140

RESULT 10
PC2060
genome polyprotein N1 - hepatitis C virus
N/Contains: envelope protein E1; nonstructural protein E2/NS1
C/Species: hepatitis C virus
C/Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 31-Dec-2004
C/Accession: PC2060
R/Li, J.S.; Vitvitski, L.; Tong, S.P.; Trepo, C.
Biochem. Biophys. Res. Commun. 199, 1474-1481, 1994
A/Title: Identification of the third major genotype of hepatitis C virus in France.
A/Reference number: PC2060; MUID:94197744; PMID:8147893
A/Accession: PC2060
A:Molecule type: mRNA
A:Residues: 1-411 <LIJ>
A:Cross-references: UNIPROT:Q81489; UNIPARC:UPI0000178524
C/Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;
F:192-383/Product: envelope protein E1 #status predicted <SPE>
F:384-411/Product: nonstructural protein E2/NS1 #status predicted <NPE>
F:196,209,234,305,325/Binding site: carbonylate (Asn) (covalent) #status predicted

Query Match      89.4%; Score 42; DB 2; Length 411;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
      |||||
Db      132 DLMGYIPLV 140

RESULT 11
S12707
genome polyprotein - hepatitis C virus (fragment)
N/Contains: core protein; envelope protein
C/Species: hepatitis C virus
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: S12707
R/Takeuchi, K.; Kubo, Y.; Boonmar, S.; Watanabe, Y.; Katayama, T.; Choo, Q.L.; Kuo, G.;
Nucleic Acids Res. 18, 4826, 1990
A/Title: Nucleotide sequence of core and envelope genes of the hepatitis C virus genome
A/Reference number: S12707; MUID:90356432; PMID:2117749
A/Accession: S12707
A:Molecule type: genomic RNA
A:Residues: 1-441 <TAK>
A:Cross-references: UNIPROT:Q81776; UNIPARC:UPI00000EFB53; EMBL:D00574; NID:G221656; PID
C:Superfamily: hepatitis C virus genome polyprotein
C/Keywords: polyprotein

Query Match      89.4%; Score 42; DB 2; Length 441;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
      |||||
Db      132 DLMGYIPLV 140

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RESULT 12
S41288
genome polyprotein - hepatitis C virus (fragment)
N/Contains: core protein; envelope protein; NS1 protein
C/Species: hepatitis C virus
C/Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 31-Dec-2004
C/Accession: S41288
R/Seelig, R.
submitted to the EMBL Data Library, December 1993
A/Reference number: S41288
A/Accession: S41288
A:Molecule type: genomic RNA
A:Residues: 1-492 <SEE>
A:Cross-references: UNIPROT:Q68870; UNIPARC:UPI0000178522; EMBL:X76918
C/Keywords: capsid protein; core protein; envelope protein; nonstructural protein; pol;
F:1-191/Product: core protein #status predicted <COR>
F:192-372/Product: envelope protein #status predicted <ENV>
F:373-492/Product: NS1 protein (fragment) #status predicted <NS1>

Query Match      89.4%; Score 42; DB 2; Length 492;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
      |||||
Db      132 DLMGYIPLV 140

RESULT 13
PC1284
genome polyprotein - hepatitis C virus (isolate HC-J4) (fragment)
C/Species: hepatitis C virus
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: PC1284
R/Okamoto, H.; Okada, S.; Sugiyama, Y.; Yotsumoto, S.; Tanaka, T.; Yoshizawa, H.; Taud;
Jpn. J. Exp. Med. 60, 167-177, 1990
A/Title: The 5'-terminal sequence of the hepatitis C virus genome.
A/Reference number: PC1284; MUID:9103116; PMID:2170712
A/Accession: PC1284
A:Molecule type: genomic RNA
A:Residues: 1-513 <OKA>
A:Cross-references: UNIPROT:Q81221; UNIPARC:UPI00000EBE30; GB:D00832; NID:G221513; PID
C:Superfamily: hepatitis C virus genome polyprotein

Query Match      89.4%; Score 42; DB 2; Length 513;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DLMGYIPAV 9
      |||||
Db      132 DLMGYIPLV 140

RESULT 14
A44150
structural protein - hepatitis C virus
C/Species: hepatitis C virus
C/Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 31-Dec-2004
C/Accession: A44150
R/Ching, W.M.; Wychowski, C.; Beach, M.J.; Wang, H.; Davies, C.L.; Carl, M.; Bradley, I
Proc. Natl. Acad. Sci. U.S.A. 89, 3190-3194, 1992
A/Title: Interaction of immune sera with synthetic peptides corresponding to the struct
A/Reference number: A44150; MUID:9228749; PMID:1373489
A/Accession: A44150
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: genomic RNA
A:Residues: 1-513 <CHI>
A:Cross-references: UNIPROT:Q91FE5; UNIPROT:O36579; UNIPROT:O36610; UNIPROT:Q9ELS9; UN:

Query Match      89.4%; Score 42; DB 2; Length 513;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 DLMGYIPAV 9
Db      132 DLMGYIPLV 140

RESULT 15
JQ1925
polyprotein - hepatitis C virus (isolate HCV-KF)
N:Contains: C protein; E1 protein; E2/NS1 protein
C:Species: hepatitis C virus
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: JQ1925
R:Abe, K.; Inchauspe, G.; Fujisawa, K.
J. Gen. Virol. 73, 2725-2729, 1992
A:Title: Genomic characterization and mutation rate of hepatitis C virus isolated from a
A:Reference number: JQ1925; MUID:93019030; PMID:1383400
A:Accession: JQ1925
A:Molecule type: mRNA
A:Residues: 1-520 <ABE>
A:Cross-references: UNIPROT:Q01403; UNIPARC:UPI0000131E22; DBJ:D10687; NID:g221544; PID:
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: polyprotein; transmembrane protein
F:1-191/Product: C protein #status predicted <CPR>
F:192-383/Product: E1 protein #status predicted <E1R>
F:384-520/Product: E2/NS1 protein #status predicted <E2P>

Query Match      89.4%; Score 42; DB 2; Length 520;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      1 DLMGYIPAV 9
Db      132 DLMGYIPLV 140

RESULT 16
JQ1926
polyprotein - hepatitis C virus (isolate HCV-476)
N:Contains: C protein; E1 protein; E2/NS1 protein
C:Species: hepatitis C virus
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C:Accession: JQ1926
R:Abe, K.; Inchauspe, G.; Fujisawa, K.
J. Gen. Virol. 73, 2725-2729, 1992
A:Title: Genomic characterization and mutation rate of hepatitis C virus isolated from a
A:Reference number: JQ1925; MUID:93019030; PMID:1383400
A:Accession: JQ1926
A:Molecule type: mRNA
A:Residues: 1-523 <ABE>
A:Cross-references: UNIPARC:UPI0000178525; DBJ:D10687
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: polyprotein
F:1-191/Product: C protein #status predicted <CPR>
F:192-383/Product: E1 protein #status predicted <E1R>
F:384-523/Product: E2/NS1 protein #status predicted <E2P>

Query Match      89.4%; Score 42; DB 2; Length 523;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      1 DLMGYIPAV 9
Db      132 DLMGYIPLV 140

RESULT 17
JH0711
genome polyprotein - hepatitis C virus (strain PRCl) (fragments)
N:Contains: envelope protein E1; envelope protein E2; nonstructural protein NS1; nonstru
C:Species: hepatitis C virus
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: JH0711

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R.Liu, K.; Hu, Z.; Li, H.; Prince, A.M.; Inchauspe, G.
Gene 114, 245-250, 1992
A:Title: Genomic typing of hepatitis C viruses present in China.
A:Reference number: JH0711; MUID:92290283; PMID:1318245
A:Accession: JH0711
A:Molecule type: genomic RNA
A:Residues: 1-550 <LIU>
A:Cross-references: UNIPROT:Q7L2V4; UNIPARC:UPI00001784F8; GB:M74888; GB:M74889
A>Note: the nucleotide sequence is not complete
A:Note: translation of the nucleotide sequence is not complete
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: envelope protein; glycoprotein; nonstructural protein; nucleocapsid; poly
F:1-190/Product: nucleocapsid protein C #status predicted <CPC>
F:191-380/Product: envelope protein E1 #status predicted <E1P>
F:381-514/Product: envelope protein E2 or nonstructural protein NS1 (fragment) #status
F:515-550/Product: nonstructural protein NS5 (fragment) #status predicted <NS5>
F:196,233,250,305,416,422,423,447/Binding site: carbohydrate (Asn) (covalent) #status
Query Match      89.4%; Score 42; DB 2; Length 550;
Best Local Similarity 88.9%; Pred. No. 1.9;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      1 DLMGYIPAV 9
Db      132 DLMGYIPLV 140

RESULT 18
JQ1584
genome polyprotein - hepatitis C virus (strain U.K.) (fragment)
N:Contains: core protein C; envelope protein E1; envelope protein E2; nonstructural pr
C:Species: hepatitis C virus
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: JQ1584
R:Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
J. Gen. Virol. 73, 1521-1525, 1992
A:Title: Cloning and sequencing of the structural region and expression of putative co
A:Reference number: JQ1584; MUID:92300349; PMID:1318944
A:Accession: JQ1584
A:Molecule type: genomic RNA
A:Residues: 1-640 <KUM>
A:Cross-references: UNIPROT:Q68966; UNIPARC:UPI00000EFF23; GB:X84079; NID:g6431119; PID
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: core protein; envelope protein; glycoprotein; nonstructural protein; poly
F:1-191/Product: core protein C #status predicted <CPC>
F:192-389/Product: envelope protein E1 #status predicted <E1>
F:390-640/Product: envelope protein E2 and nonstructural protein NS1 #status predicted
F:196,209,234,305,417,430,448,476,540,556,576,623/Binding site: carbohydrate (Asn) (co
Query Match      89.4%; Score 42; DB 2; Length 640;
Best Local Similarity 88.9%; Pred. No. 2.3;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      1 DLMGYIPAV 9
Db      132 DLMGYIPLV 140

RESULT 19
S18032
genome polyprotein - hepatitis C virus (isolate JK4) (fragment)
N:Contains: core protein; envelope protein E1; nonstructural protein E2; NS1/E2 protein
C:Species: hepatitis C virus
A:Variety: isolate JK4
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: S18032
R:Honda, M.; Kaneko, S.; Maeashi, U.; Kobayashi, K.; Murakami, S.
submitted to the ENBL Data Library, September 1991
A:Description: Sequence analysis of putative structural regions of Hepatitis C Virus i
A:Reference number: S18029
A:Accession: S18032
A:Molecule type: genomic RNA
A:Residues: 1-782 <HON>

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A;Cross-references: UNIPROT:Q68952; UNIPARC:UPI0000178521; EMBL:X61594
 A;Experimental source: isolate JK4
 C;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural
 F;1-191/Product: core protein #status predicted <MAT1>
 F;192-383/Product: envelope protein 1 #status predicted <MAT2>
 F;384-733/Product: NS1/E2 protein #status predicted <MAT3>
 F;734-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>

Query Match 89.4%; Score 42; DB 2; Length 782;
 Best Local Similarity 88.9%; Pred. No. 2.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 |||||
 DB 132 DLMGYIPLV 140

RESULT 20
 S18031 genome polyprotein - hepatitis C virus (isolate JK2) (fragment)
 N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
 C;Species: hepatitis C virus
 A;Variety: isolate JK2
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C;Accession: S18031
 R;Honda, M.; Kaneo, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
 submitted to the EMBL Data Library, September 1991
 A;Description: Sequence analysis of putative structural regions of Hepatitis C Virus iso
 A;Reference number: S18029
 A;Accession: S18031
 A;Molecule type: genomic RNA
 A;Residues: 1-782 <HON>
 A;Cross-references: UNIPROT:Q68950; UNIPARC:UPI0000178520; EMBL:X61593
 A;Experimental source: isolate JK2
 C;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural
 F;1-191/Product: core protein #status predicted <MAT1>
 F;192-383/Product: envelope protein 1 #status predicted <MAT2>
 F;384-733/Product: NS1/E2 protein #status predicted <MAT3>
 F;734-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>

Query Match 89.4%; Score 42; DB 2; Length 782;
 Best Local Similarity 88.9%; Pred. No. 2.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 |||||
 DB 132 DLMGYIPLV 140

RESULT 21
 S19875 genome polyprotein - hepatitis C virus (isolate JK3) (fragment)
 N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
 C;Species: hepatitis C virus
 A;Variety: isolate JK3
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C;Accession: S19875
 R;Honda, M.; Kaneo, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
 submitted to the EMBL Data Library, September 1991
 A;Description: Sequence analysis of putative structural regions of Hepatitis C Virus iso
 A;Reference number: S18029
 A;Accession: S19875
 A;Molecule type: genomic RNA
 A;Residues: 1-782 <HON>
 A;Cross-references: UNIPROT:Q68951; UNIPARC:UPI00000F03B9; EMBL:X61592; NID:G59482; PIDN
 A;Experimental source: isolate JK3
 C;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural
 F;1-191/Product: core protein #status predicted <MAT1>
 F;192-383/Product: envelope protein 1 #status predicted <MAT2>
 F;384-733/Product: NS1/E2 protein #status predicted <MAT3>

F;734-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>

Query Match 89.4%; Score 42; DB 2; Length 782;
 Best Local Similarity 88.9%; Pred. No. 2.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 |||||
 DB 132 DLMGYIPLV 140

RESULT 22
 PN0677 hypochemical protein 787 - hepatitis C virus (fragment)
 C;Species: hepatitis C virus
 C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
 C;Accession: PN0677
 R;Cho, S.H.; Yoon, J.I.; Chang, J.E.; Ahn, B.M.; Lee, C.H.; Lee, Y.I.
 Biochem. Biophys. Res. Commun. 196:780-788, 1993
 A;Title: Genomic typing of hepatitis C viruses from Korean patients: Implications of 9
 A;Reference number: PN0677; MUID:94059104; PMID:8240354
 A;Accession: PN0677
 A;Molecule type: mRNA
 A;Residues: 1-787 <CHO>
 A;Cross-references: UNIPROT:Q08244; UNIPARC:UPI00000F6521; GB:L20498; NID:GL381031; PI
 C;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: glycoprotein; nonstructural protein
 F;196,209,234,250,305,325,421,427,452,536,544,560,580,627,649/Binding site: carbohydra

Query Match 89.4%; Score 42; DB 2; Length 787;
 Best Local Similarity 88.9%; Pred. No. 2.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 |||||
 DB 132 DLMGYIPLV 140

RESULT 23
 PC2219 polypeptide - hepatitis C virus (type 5a) (fragments)
 N;Contains: core protein; E1 (carboxyl end); E2/NS1 (amino end); NS3 protein; NS4A pro
 C;Species: hepatitis C virus
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 31-Dec-2004
 C;Accession: PC2219
 R;Stuyver, L.; Arnhem, W.V.; Wyseur, A.; Maertens, G.
 Biochem. Biophys. Res. Commun. 202:1308-1314, 1994
 A;Title: Cloning and phylogenetic analysis of the core, E2, and NS3/NS4 regions of the
 A;Reference number: PC2219; MUID:94338342; PMID:7520237
 A;Accession: PC2219
 A;Molecule type: mRNA
 A;Residues: 1-876 <STU>
 A;Cross-references: UNIPROT:Q81242; UNIPARC:UPI00001784FF; GB:L29577; GB:L29578; GB:L2
 A;Experimental source: serum
 C;Keywords: glycoprotein
 F;1-191/Product: core #status predicted <COE>
 F;68-78/Region: variable
 F;192-247/Product: E1 (carboxyl end) #status predicted <ERE>
 F;248-411/Product: E2/NS1 (amino end) #status predicted <ENR>
 F;248-338/Region: E2
 F;339-411/Region: NS1 (amino end)
 F;412-783/Product: NS3 #status predicted <NSR>
 F;784-837/Product: NS4A #status predicted <NSA>
 F;838-876/Product: NS4B #status predicted <NSB>
 F;288,287,294,312,340/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.4%; Score 42; DB 2; Length 876;
 Best Local Similarity 88.9%; Pred. No. 3.1;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
 |||||
 DB 132 DLMGYIPLV 140

RESULT 24

A45573

genome polyprotein - hepatitis C virus (strain JT)
N:Contains: capsid protein C; envelope protein M; hepatitis C virus (strain JT) (nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5)
C:Species: hepatitis C virus
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: A45573

R:Panaka, T.; Kato, N.; Nakagawa, M.; Ootsuyama, Y.; Cho, M.J.; Nakazawa, T.; Hijioka, T. Virus Res. 23, 39-53, 1992

A:Title: Molecular cloning of hepatitis C virus genome from a single Japanese carrier: A:Reference number: A45573; MUID:92295714; PMID:1318627

A:Accession: A45573

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-3010 <TAN>

A:Cross-references: UNIPROT:Q00269; UNIPARC:UPI0000131E29; GB:D011171; NID:g22

A:Experimental source: HCV-JT

A>Note: sequence extracted from NCBI backbone (NCBI:106206, NCBI:106207)

C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serin

F:2-115/Product: capsid protein C #status predicted <CPC>

F:116-191/Product: envelope protein M #status predicted <EPM>

F:192-389/Product: major envelope protein E #status predicted <MEP>

F:730-1006/Product: nonstructural protein NS1 #status predicted <NS1>

F:1007-1615/Product: hepatitis C virus NS2 #status predicted <NS2>

F:1230-1237/Region: nucleotide-binding motif A (P-loop)

F:1312-1317/Region: nucleotide-binding motif A (P-loop)

F:1316-1319/Region: DEXH motif

F:1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>

F:1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>

F:2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>

Query Match

Best Local Similarity 89.4%; Score 42; DB 1; Length 3010;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9

Db 132 DLMGYIPLV 140

RESULT 25

GNWVCJ

genome polyprotein - hepatitis C virus (strain J)
N:Contains: capsid protein C; envelope protein M; major envelope protein E; nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5

C:Species: hepatitis C virus
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: A39253; PS0086

R:Kato, N.; Hijioka, M.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S.; Sugimura, T.; Shimoto Proc. Natl. Acad. Sci. U.S.A. 87, 9524-9528, 1990

A:Title: Molecular cloning of the human hepatitis C virus genome from Japanese patients A:Reference number: A39253; MUID:91088550; PMID:2175903

A:Accession: A39253

A:Molecule type: genomic RNA

A:Residues: 1-3010 <KAT>

A:Cross-references: UNIPROT:P26662; UNIPARC:UPI0000131E28; GB:D90208; NID:g221610; PIDN: R:Kato, N.; Ohkoshi, S.; Shimotohno, K. Proc. Jpn. Acad. 65B, 219-223, 1989

A:Title: Japanese isolates of the non-A, non-B hepatitis viral genome show sequence vari A:Reference number: PS0085

A:Accession: PS0086

A:Molecule type: genomic RNA

A:Residues: 2650-2707 <KAT>

A:Cross-references: UNIPARC:UPI00000F7365

A:Experimental source: Japanese isolate

A:Comment: The cleavage sites of this polyprotein have not been determined.

C:Superfamily: hepatitis C virus genome polyprotein

C:Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serin

F:2-115/Product: capsid protein C #status predicted <CPC>
F:116-191/Product: envelope protein M #status predicted <EPM>
F:192-389/Product: major envelope protein E #status predicted <MEP>
F:730-1006/Product: nonstructural protein NS1 #status predicted <NS1>
F:1007-1615/Product: hepatitis C virus NS2 #status predicted <NS2>
F:1230-1237/Region: nucleotide-binding motif A (P-loop)
F:1312-1317/Region: nucleotide-binding motif A (P-loop)
F:1316-1319/Region: DEXH motif

F:1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F:1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F:2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F:196-209, 234, 250, 305, 325, 417, 423, 430, 448, 532, 556, 576, 623, 645, 1213, 1255, 2041, 2077, 2240

Query Match 89.4%; Score 42; DB 1; Length 3010;

Best Local Similarity 88.9%; Pred. No. 11;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9

Db 132 DLMGYIPLV 140

RESULT 26

GNWVC

genome polyprotein - hepatitis C virus
N:Contains: capsid protein C; envelope protein M; hepatitis C virus (strain JT) (nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5)

C:Species: hepatitis C virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: A38465

R:Takamizawa, A.; Mori, C.; Fuke, I.; Manabe, S.; Murakami, S.; Fujita, J.; Onishi, E. J. Virol. 65, 1105-1113, 1991

A:Title: Structure and organization of the hepatitis C virus genome isolated from human A:Reference number: A38465; MUID:91140698; PMID:1847440

A:Accession: A38465

A:Molecule type: genomic RNA

A:Residues: 1-3010 <TAK>

A:Cross-references: UNIPROT:P26663; UNIPARC:UPI0000131E1C; EMBL:M58335; NID:g329770; P C:Superfamily: hepatitis C virus genome polyprotein

C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructu F:2-115/Product: capsid protein C #status predicted <CPC>

F:116-191/Product: envelope protein M #status predicted <EPM>
F:192-389/Product: major envelope protein E #status predicted <MEP>

F:730-1006/Product: nonstructural protein NS1 #status predicted <NS1>
F:1007-1615/Product: hepatitis C virus NS2 #status predicted <NS2>

F:1230-1237/Region: nucleotide-binding motif A (P-loop)
F:1312-1317/Region: nucleotide-binding motif A (P-loop)

F:1316-1319/Region: DEXH motif
F:1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>

F:1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F:2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>

F:196-209, 234, 250, 305, 325, 417, 423, 430, 448, 532, 540, 556, 576, 623, 645, 1213, 1255, 2041, 2077,

Query Match 89.4%; Score 42; DB 1; Length 3010;

Best Local Similarity 88.9%; Pred. No. 11;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9

Db 132 DLMGYIPLV 140

RESULT 27

GNWVTW

genome polyprotein - hepatitis C virus (strain Taiwan)
N:Contains: capsid protein C; envelope protein M; hepatitis C virus (strain Taiwan) (nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5)

C:Species: hepatitis C virus
A>Note: host Homo sapiens (man)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C:Accession: A40244

R.; Chen, P. J.; Lin, M. H.; Tai, K. F.; Liu, P. C.; Lin, C. J.; Chen, D. S.
 Virology 188, 102-113, 1992
 A>Title: The Taiwanese hepatitis C virus genome: sequence determination and mapping the
 A:Reference number: A40244; MUID:92230206; PMID:1314449
 A:Accession: A40244
 A:Molecule type: Genomic RNA
 A:Residues: 1-3010 <CHS>
 A:Cross-references: UNIPROT:P29846; UNIPARC:UPI0000131E2B; GB:M84754
 C:Superfamily: hepatitis C virus genome polyprotein
 C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructural
 F:1-115/Product: capsid protein C #status predicted <CPC>
 F:116-191/Product: envelope protein M #status predicted <EPM>
 F:192-389/Product: major envelope protein E #status predicted <ME>
 F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>
 F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
 F:1007-1615/Product: hepatitis virus #status predicted <NS3>
 F:1230-1237/Region: nucleotide-binding motif A (P-loop)
 F:1312-1317/Region: nucleotide-binding motif B
 F:1316-1319/Region: DEXH motif
 F:1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
 F:1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
 F:2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
 F:196,209,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,2077

Query Match 89.4%; Score 42; DB 1; Length 3010;
 Best Local Similarity 88.9%; Pred. No. 11; Mismatches 0; Gaps 0;
 Matches 8; Conservative 0; Indels 1; Indels 0;

QY 1 DLMGYIPAV 9
 |||||
 DB 132 DLMGYIPLV 140

RESULT 28
 S18030
 genome polyprotein - hepatitis C virus (isolate JK1)
 N:Contains: capsid protein C; envelope protein M; hepatitis virus (EC 3.4.21.98) (nonstructural
 protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
 C:Species: hepatitis C virus
 C:Date: 19-May-2000 #sequence revision 19-May-2000 #text_change 09-Jul-2004
 R:Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
 submitted to the EMBL Data Library, September 1991
 A:Description: A whole genome of hepatitis C virus cDNA was isolated from a single patient
 A:Reference number: S18028
 A:Accession: S18030
 A:Molecule type: Genomic RNA
 A:Residues: 1-3010 <HON>
 A:Cross-references: UNIPROT:Q68949; UNIPARC:UPI00000F2A81; EMBL:X61596; NID:G59478; PIDN
 A:Experimental source: isolate JK1 from an individual
 R:Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
 Arch. Virol. 128, 163-169, 1993
 A>Title: Sequence analysis of putative structural regions of hepatitis C virus isolated
 A:Reference number: A48332; MUID:93119270; PMID:8380322
 A:Accession: S33570
 A:Molecule type: Genomic RNA
 A:Residues: 1-547, 'T', 549-621, 'V', 623-624, 'S', 626-652, 'DL', 655-761, 'T', 763-782 <HOW>
 A:Cross-references: UNIPARC:UPI00001749FF; EMBL:X61591
 A>Note: this sequence is inconsistent with the nucleotide translation
 A>Note: the authors translated the codon AGG for residue 43 as Pro, TGG for residue 320
 as Trp, and TTC for residue 771 as Ser
 A>Note: sequence extracted from NCBI backbone (NCBI:121747, NCBI:121748)
 C:Superfamily: hepatitis C virus genome polyprotein
 C:Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serin
 F:2-115/Product: capsid protein C #status predicted <CPC>
 F:116-191/Product: envelope protein M #status predicted <EPM>
 F:192-389/Product: major envelope protein E #status predicted <ME>
 F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>
 F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
 F:1007-1615/Product: hepatitis virus #status predicted <NS3>
 F:1230-1237/Region: nucleotide-binding motif A (P-loop)
 F:1312-1317/Region: nucleotide-binding motif B

F:1316-1319/Region: DEXH motif
 F:1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
 F:1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
 F:2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
 F:196,209,234,250,305,417,423,448,532,540,556,576,623,645/Binding site: carbohydrate

Query Match 89.4%; Score 42; DB 1; Length 3010;
 Best Local Similarity 88.9%; Pred. No. 11; Mismatches 0; Gaps 0;
 Matches 8; Conservative 0; Indels 1; Indels 0;

QY 1 DLMGYIPAV 9
 |||||
 DB 132 DLMGYIPLV 140

RESULT 29
 GNVVCH
 genome polyprotein - hepatitis C virus (strain HCV-1)
 N:Contains: capsid protein C; envelope protein M; hepatitis virus (EC 3.4.21.98) (nonstructural
 protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
 C:Species: hepatitis C virus
 C:Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
 C:Accession: A39166; PQ0403; PQ0404
 R:Choo, Q. L.; Richman, K. H.; Han, J. H.; Berger, K.; Lee, C.; Dong, C.; Gallegos, C.; C
 Proc. Natl. Acad. Sci. U.S.A. 88, 2451-2455, 1991
 A>Title: Genetic organization and diversity of the hepatitis C virus.
 A:Reference number: A39166; MUID:91172826; PMID:1848704
 A:Accession: A39166
 A:Molecule type: mRNA
 A:Residues: 1-3011 <CHO>
 A:Cross-references: UNIPROT:P26664; UNIPARC:UPI0000131B19; GB:M62321; NID:G329873; PID
 R:Chan, S. W.; McOmish, F.; Holmes, E. C.; Dow, B.; Peutherer, J. F.; Follett, E.; Yap, P
 J. Gen. Virol. 73, 1131-1141, 1992
 A>Title: Analysis of a new hepatitis C virus type and its phylogenetic relationship to
 A:Reference number: PQ0393; MUID:92268871; PMID:1316939
 A:Accession: PQ0403
 A:Molecule type: Genomic RNA
 A:Residues: 1577-1633 <CHA>
 A:Cross-references: UNIPARC:UPI0000174A00; DBJ:D10128
 A:Experimental source: isolates E-b16
 A:Accession: PQ0404
 A>Status: preliminary
 A:Molecule type: Genomic RNA
 A:Residues: 1577-1633 <CH2>
 A:Cross-references: UNIPARC:UPI0000174A00
 A:Experimental source: isolates E-b17
 C:Superfamily: hepatitis C virus genome polyprotein
 C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructu
 F:1-115/Product: capsid protein C #status predicted <CPC>
 F:116-191/Product: envelope protein M #status predicted <EPM>
 F:192-389/Product: major envelope protein E #status predicted <ME>
 F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>
 F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
 F:1007-1615/Product: hepatitis virus #status predicted <NS3>
 F:1230-1237/Region: nucleotide-binding motif A (P-loop)
 F:1312-1317/Region: nucleotide-binding motif B
 F:1316-1319/Region: DEXH motif
 F:1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
 F:1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
 F:2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
 F:196,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,1255,2041,2077,

Query Match 89.4%; Score 42; DB 1; Length 3011;
 Best Local Similarity 88.9%; Pred. No. 11; Mismatches 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 1; Indels 0;

QY 1 DLMGYIPAV 9
 |||||
 DB 132 DLMGYIPLV 140

RESULT 30
 GNVVCH

F;116-191/Product:	envelope protein M #status predicted <EPM>
F;192-389/Product:	major envelope protein E #status predicted <ME>
F;390-729/Product:	nonstructural protein NS1 #status predicted <NS1>
F;730-1006/Product:	nonstructural protein NS2 #status predicted <NS2>
F;1007-1615/Product:	hepacivirin #status predicted <NS3>
F;1230-1237/Region:	nucleotide-binding motif A (P-loop)
F;1312-1317/Region:	nucleotide-binding motif B
F;1316-1319/Region:	DEXH motif
F;1616-1862/Product:	nonstructural protein NS4a #status predicted <N4A>
F;1863-2013/Product:	nonstructural protein NS4b #status predicted <N4B>
F;2014-3011/Product:	nonstructural protein NS5 #status predicted <NS5>

Query Match	89.4%; Score 42; DB 1; Length 3011;
Best Local Similarity	88.9%; Pred. No. 11;
Matches	8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1 DLMGYIPAV 9
Db	132 DLMGYIFLV 140

RESULT 32

JE0395

Phospho-beta-galactosidase I - Lactobacillus gasseri

C:Species: Lactobacillus gasseri

C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004

C:Accession: JE0395

R:Saito, T.; Suzuki, M.; Konno, K.; Kitazawa, H.; Kawai, Y.; Itoh, T.; Kamio, Y.

Biosci. Biotechnol. Biochem. 62, 2318-2327, 1998

A>Title: Molecular cloning and sequencing of two phospho-beta-galactosidase I and II genes from *Lactobacillus gasseri*

A:Reference number: JE0395; MUID:99138205; PMID:9972258

A:Accession: JE0395

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-482 <SAI>

A:Cross-references: UNIPROT.O06532; UNIPARC.UPI00000BABA7; DDBJ:AB003927

C:Superfamily: Agrobacterium beta-glucosidase

```

Query Match      78.7%; Score 37; DB 2; Length 482;
Best Local Similarity 85.7%; Pred. No. 17;
Matches        6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy    1 DLMGYIP 7
      |||||
Db    420 DLMGYLP 426

RESULT 33
Tl3006
betaine aldehyde dehydrogenase homolog T24C20.50 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: Tl3006
R:Choigne, N.; Robert, C.; Brottier, P.; Wincker, P.; Catolico, L.; Artiguenave, F.; et al.
submitted to the Protein Sequence Database, July 1999
A:Reference number: Tl7586
A:Accession: Tl3006
A:Molecule type: DNA
A:Residues: 1-503 <CHO>
A:Cross-references: UNIPROT.Q9STS1; UNIPARC.UPI00000A828C; EMBL.AL096856; GSFPDB.GN0006.
A:Experimental source: cultivar Columbia; BAC clone T24C20
C:Genetics:
A:Gene: ATSP.T24C20.50
A:Map position: 3
A:Introns: 37/1; 84/3; 111/3; 161/2; 192/2; 233/3; 255/3; 278/1; 303/3; 341/3; 367/3;
C:Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
F;46-314/Domain: aldehyde dehydrogenase homology <ALD>

Query Match      78.7%; Score 37; DB 2; Length 503;
Best Local Similarity 75.0%; Pred. No. 18;
Matches        6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy    1 DLMGYIPA 8

```


Db 34 DIIGYIPA 41
|:|||||
|:|||||

RESULT 34
JC5620
genome polyprotein - hepatitis C virus (isolate EUH1480)
N:Contains: capsid protein C; envelope protein M; hepatitis C virus (nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C:Species: hepatitis C virus
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: JC5620
R:Chamberlain, R.W.; Adams, N.J.; Taylor, L.A.; Simmonds, P.; Elliott, R.M.
Biochem. Biophys. Res. Commun. 236, 44-49, 1997
A:Title: The complete coding sequence of hepatitis C virus genotype 5a, the predominant
A:Reference number: JC5620; MUID:97366593; PMID:9223423
A:Accession: JC5620
A:Molecule type: mRNA
A:Residues: 1-3014 <CHA>
A:Cross-references: UNIPROT:O39928; UNIPARC:UPI0000174A01; GB:Y13184
A:Experimental source: genotype 5a, which predominates in South Africa
A:Note: the translation of the nucleotide sequence is not complete in this paper
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serin
F:2-115/Product: capsid protein C #status predicted <CPC>
F:116-191/Product: envelope protein M #status predicted <EPM>
F:132-389/Product: major envelope protein E #status predicted <MEE>
F:384-408/Region: hypervariable #status predicted
F:390-730/Product: nonstructural protein NS1 #status predicted <NS1>
F:731-1007/Product: nonstructural protein NS2 #status predicted <NS2>
F:1008-1616/Product: hepatitis C virus genome polyprotein #status predicted <NS3>
F:1231-1238/Region: nucleotide-binding motif A (P-loop)
F:1313-1318/Region: nucleotide-binding motif B
F:1317-1320/Region: DEXH motif
F:1617-1863/Product: nonstructural protein NS4a #status predicted <N4A>
F:1864-2014/Product: nonstructural protein NS4b #status predicted <N4B>
F:2015-3014/Product: nonstructural protein NS5 #status predicted <NS5>
F:2210-2249/Region: interferon sensitivity determining #status predicted
Query Match 76.6%; Score 36; DB 1; Length 3014;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 LMGYIPAV 9
|:|||||
|:|||||
Db 133 LMGYIPLV 140

RESULT 35
T03534
precorrin-3 methylase (EC 2.1.1.1) - Rhodobacter capsulatus
C:Species: Rhodobacter capsulatus
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03534
R:Vicek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haseelkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A:Title: Sequence of a 189-Kb segment of the chromosome of Rhodobacter capsulatus SB1003
A:Reference number: Z14955; MUID:97404404; PMID:9256491
A:Accession: T03534
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-245 <VLC>
A:Cross-references: UNIPROT:O68097; UNIPARC:UPI00000BDIA3; EMBL:AF010496; NID:g3128256;
C:Genetics:
A:Map position: 1
C:Superfamily: precorrin-3B C17-methyltransferase
C:Keywords: methyltransferase
Query Match 74.5%; Score 35; DB 2; Length 245;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 0;
Qy 1 DLMGYIPAV 9

Db 31 DIVGYIPV 39
|:|||||
|:|||||

RESULT 36
T29715
hypothetical protein K02H8.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29715
R:Latreille, P.; Bradshaw, H.
submitted to the EMBL Data Library, August 1996
A:Description: The sequence of C. elegans cosmid K02H8.
A:Reference number: Z20671
A:Accession: T29715
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-284 <LAT>
A:Cross-references: UNIPROT:Q94250; UNIPARC:UPI000012ED34; EMBL:U67957; PIDN:RAB07587;
A:Experimental source: strain Bristol N2; clone K02H8
C:Genetics:
A:Gene: CESP:K02H8.1
A:Map position: X
A:Introns: 40/3; 83/3; 138/3; 156/3; 231/3
Query Match 74.5%; Score 35; DB 2; Length 284;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 LMGYIPAV 9
|:|||||
|:|||||
Db 267 LQGYVPAV 274

RESULT 37
E64300
formate dehydrogenase (EC 1.2.1.2) beta chain - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: E64300
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A.; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: E64300
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-379 <BUL>
A:Cross-references: UNIPROT:Q60316; UNIPARC:UPI0000012A5DE; GB:U67459; GB:L77117; NID:g:
C:Genetics:
A:Map position: REV7250-6111
C:Superfamily: formate dehydrogenase chain B; ferredoxin 2[4Fe-4S] homology
C:Keywords: oxidoreductase
F:273-348/Domain: ferredoxin 2[4Fe-4S] homology <FER>
Query Match 74.5%; Score 35; DB 2; Length 379;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 DLMGYIPAV 9
|:|||||
|:|||||
Db 359 DTLGYPGV 367

RESULT 38
H81805
DNA topoisomerase IV subunit A (EC 5.99.1.-) NMA1802 [imported] - Neisseria meningitidis
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-Oct-2004
C:Accession: H81805

R.Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
 A:Reference number: AB1775, MUID:20222556; PMID:10761919
 A:Accession: HB1805
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-765 <PAR>
 A:Cross-references: UNIPROT:Q9JTF1; UNIPARC:UPI00000C4C9E; GB:AL162757; GB:AL157959; NID
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: parC; NMA1802
 C:Superfamily: Type II topoisomerase, subunit A; phage T4 DNA topoisomerase (ATP-hydroly
 C:Keywords: isomerase

Query Match 74.5%; Score 35; DB 2; Length 765;
 Best Local Similarity 87.5%; Pred. No. 69;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPA 8
 ||| ||||
 Db 209 DLMQYIPA 216

RESULT 39
 GB1064
 topoisomerase IV chain A NMB1605 [imported] - *Neisseria meningitidis* (strain MC58 serogr
 C:Species: *Neisseria meningitidis*
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
 C:Accession: GB1064
 Rietelink, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
 A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A:Reference number: AB1000; MUID:20175755; PMID:10710307
 A:Accession: GB1064
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-767 <TET>
 A:Cross-references: UNIPROT:Q9JTF6; UNIPARC:UPI00000C4752; GB:AE002511; GB:AE002098; NID
 A:Experimental source: serogroup B, strain MC58
 C:Genetics:
 A:Gene: NMB1605
 C:Superfamily: Type II topoisomerase, subunit A; phage T4 DNA topoisomerase (ATP-hydroly

Query Match 74.5%; Score 35; DB 2; Length 767;
 Best Local Similarity 87.5%; Pred. No. 70;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPA 8
 ||| ||||
 Db 211 DLMQYIPA 218

RESULT 40
 S60780
 topoisomerase IV chain A - *Neisseria gonorrhoeae*
 C:Species: *Neisseria gonorrhoeae*
 C:Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 05-Oct-2004
 C:Accession: S60780
 R.Belland, R.J.; Morrison, S.G.; Ison, C.; Huang, W.M.
 Mol. Microbiol. 14, 371-380, 1994
 A:Title: *Neisseria gonorrhoeae* acquires mutations in analogous regions of *gyrA* and *parC*
 A:Reference number: S60779; MUID:95131758; PMID:7830580
 A:Accession: S60780
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-768 <BEL>
 A:Cross-references: UNIPROT:P48374; UNIPARC:UPI0000131339; EMBL:U08907; NID:9529409; PID
 C:Superfamily: Type II topoisomerase, subunit A; phage T4 DNA topoisomerase (ATP-hydroly

F:5-243/Domain: phage T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology <T4
 Query Match 74.5%; Score 35; DB 2; Length 768;
 Best Local Similarity 87.5%; Pred. No. 70;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPA 8
 ||| ||||
 Db 211 DLMQYIPA 218

Search completed: January 20, 2006, 22:42:00
 Job time : 18 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 22:41:39 ; Search time 116 Seconds

(without alignments)
32.418 Million cell updates/sec

Title: US-10-770-117-1

Perfect score: 47

Sequence: 1 DLMGYIPAV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

*Database :

Published Applications AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	47	100.0	9	US-10-114-823B-3
2	47	100.0	5	US-10-770-117-1
3	47	100.0	9	US-11-082-595-3
4	47	100.0	191	US-10-770-117-2
5	43	91.5	190	US-10-450-649-8
6	43	91.5	193	US-10-651-165-203
7	43	91.5	209	US-10-128-590-89
8	43	91.5	209	US-10-128-590-90
9	43	91.5	209	US-10-128-590-94
10	43	91.5	209	US-10-128-590-95
11	43	91.5	209	US-10-128-587A-89
12	43	91.5	209	US-10-128-587A-90
13	43	91.5	209	US-10-128-587A-94
14	43	91.5	209	US-10-128-587A-95
15	43	91.5	304	US-10-651-165-204
16	43	91.5	318	US-09-851-138-76
17	43	91.5	319	US-09-851-138-18
18	43	91.5	319	US-09-851-138-44
19	43	91.5	319	US-09-899-046-144
20	43	91.5	319	US-09-878-281-144
21	43	91.5	319	US-09-873-224-144
22	43	91.5	319	US-10-651-165-202
23	43	91.5	319	US-10-651-165-206
24	43	91.5	319	US-10-651-165-217
25	43	91.5	319	US-10-651-165-228
26	43	91.5	319	US-10-651-165-230
27	43	91.5	450	US-10-651-165-200

28	43	91.5	450	4	US-10-651-165-201	Sequence 201, App
29	43	91.5	2940	4	US-10-226-622A-13	Sequence 13, Appl
30	42	89.4	9	2	US-08-854-825-54	Sequence 54, Appl
31	42	89.4	9	3	US-09-894-018-212	Sequence 212, App
32	42	89.4	9	4	US-10-128-711-51	Sequence 51, Appl
33	42	89.4	9	4	US-10-128-711-130	Sequence 130, App
34	42	89.4	9	4	US-10-114-823B-20	Sequence 20, Appl
35	42	89.4	9	4	US-10-371-525-255	Sequence 255, App
36	42	89.4	9	4	US-10-371-069-255	Sequence 255, App
37	42	89.4	9	4	US-10-371-645-255	Sequence 255, App
38	42	89.4	9	4	US-10-371-260-255	Sequence 255, App
39	42	89.4	9	4	US-10-367-580-74	Sequence 74, Appl
40	42	89.4	9	4	US-10-367-593-74	Sequence 74, Appl
41	42	89.4	9	4	US-10-367-594-74	Sequence 74, Appl
42	42	89.4	9	4	US-10-367-654-74	Sequence 74, Appl
43	42	89.4	9	4	US-10-367-658-74	Sequence 74, Appl
44	42	89.4	9	4	US-10-367-668-74	Sequence 74, Appl
45	42	89.4	9	4	US-10-440-390-2	Sequence 2, Appl
46	42	89.4	9	4	US-10-367-674-74	Sequence 74, Appl
47	42	89.4	9	4	US-10-777-053-199	Sequence 199, App
48	42	89.4	9	4	US-10-777-053-200	Sequence 200, App
49	42	89.4	9	4	US-10-777-053-426	Sequence 426, App
50	42	89.4	9	4	US-10-837-217-199	Sequence 199, App
51	42	89.4	9	4	US-10-837-217-200	Sequence 200, App
52	42	89.4	9	4	US-10-837-217-426	Sequence 426, App
53	42	89.4	9	5	US-10-474-960A-212	Sequence 212, App
54	42	89.4	9	5	US-10-481-696-19	Sequence 19, Appl
55	42	89.4	9	5	US-10-770-117-3	Sequence 3, Appl
56	42	89.4	9	5	US-10-776-521B-53	Sequence 53, Appl
57	42	89.4	9	5	US-10-820-067A-53	Sequence 53, Appl
58	42	89.4	9	6	US-11-082-595-20	Sequence 20, Appl
59	42	89.4	10	2	US-08-854-825-1	Sequence 1, Appl
60	42	89.4	10	4	US-10-777-053-109	Sequence 109, App
61	42	89.4	10	4	US-10-837-217-109	Sequence 109, App
62	42	89.4	10	5	US-10-931-566-26	Sequence 26, Appl
63	42	89.4	15	4	US-10-103-395-172	Sequence 172, App
64	42	89.4	15	4	US-10-268-561-14	Sequence 14, Appl
65	42	89.4	15	4	US-10-268-569-14	Sequence 14, Appl
66	42	89.4	20	3	US-09-894-018-4	Sequence 4, Appl
67	42	89.4	20	4	US-10-114-823B-2	Sequence 2, Appl
68	42	89.4	20	4	US-10-651-165-10	Sequence 10, Appl
69	42	89.4	20	5	US-10-474-960A-4	Sequence 4, Appl
70	42	89.4	20	6	US-11-082-595-2	Sequence 2, Appl
71	42	89.4	21	3	US-09-894-018-3	Sequence 3, Appl
72	42	89.4	21	5	US-10-474-960A-3	Sequence 3, Appl
73	42	89.4	22	4	US-10-296-558-7	Sequence 7, Appl
74	42	89.4	24	4	US-10-651-165-216	Sequence 216, App
75	42	89.4	25	3	US-09-891-983A-31	Sequence 31, Appl
76	42	89.4	25	3	US-09-891-983A-32	Sequence 32, Appl
77	42	89.4	25	4	US-10-173-480-58	Sequence 58, Appl
78	42	89.4	25	4	US-10-173-480-59	Sequence 59, Appl
79	42	89.4	25	4	US-10-753-910-58	Sequence 58, Appl
80	42	89.4	30	4	US-10-753-910-59	Sequence 59, Appl
81	42	89.4	30	4	US-10-296-734-424	Sequence 424, App
82	42	89.4	37	4	US-10-651-165-281	Sequence 281, App
83	42	89.4	107	5	US-09-894-018-103	Sequence 103, App
84	42	89.4	130	3	US-10-474-960A-103	Sequence 103, App
85	42	89.4	130	5	US-09-894-018-99	Sequence 99, Appl
86	42	89.4	150	3	US-10-474-960A-99	Sequence 99, Appl
87	42	89.4	151	3	US-09-306-780-6	Sequence 6, Appl
88	42	89.4	151	4	US-10-292-129-14	Sequence 14, Appl
89	42	89.4	166	3	US-09-851-138-66	Sequence 66, Appl
90	42	89.4	166	3	US-09-899-046-152	Sequence 152, App
91	42	89.4	166	3	US-09-899-046-154	Sequence 154, App
92	42	89.4	166	3	US-09-898-046-194	Sequence 194, App
93	42	89.4	166	3	US-09-878-281-152	Sequence 152, App
94	42	89.4	166	3	US-09-878-281-164	Sequence 164, App
95	42	89.4	166	3	US-09-878-281-194	Sequence 194, App
96	42	89.4	166	3	US-09-873-224-152	Sequence 152, App
97	42	89.4	166	3	US-09-873-224-164	Sequence 164, App
98	42	89.4	169	3	US-09-873-224-194	Sequence 194, App
99	42	89.4	169	3	US-09-899-046-42	Sequence 42, Appl
100	42	89.4	169	3	US-09-899-046-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-10-114-823B-3
; Sequence 3, Application US/10114823B
; Publication No. US20030099663A1
; GENERAL INFORMATION:
; APPLICANT: FLEITMANN, JULIA-KRISTINA
; APPLICANT: MATTNER, FRANK
; APPLICANT: BUSCHLE, MICHAEL
; APPLICANT: MELLING, JACK
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING AN ANTIGEN
; FILE REFERENCE: SONN:016US
; CURRENT APPLICATION NUMBER: US/10/114,823B
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: PCT/EP00/09657
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: A-1680/99
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-114-823B-3

Query Match 100.0%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 1 DLMGYIPAV 9

RESULT 2
US-10-770-117-1
; Sequence 1, Application US/10770117
; Publication No. US20050129705A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States, as represented by the
; APPLICANT: Secretary, Dept. of
; APPLICANT: Health and Human Services
; APPLICANT: Berzofsky, Jay A.
; APPLICANT: Sarobe, Pablo
; APPLICANT: Pendleton, C. David
; APPLICANT: Feinstein, Stephen M.
; APPLICANT: Arichi, Tatsumi
; APPLICANT: Major, Marian E.
; TITLE OF INVENTION: MODIFIED HCV PEPTIDE VACCINES
; FILE REFERENCE: 14014.0347/P
; CURRENT APPLICATION NUMBER: US/10/770,117
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: US/09/763,260
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/097,446
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./Note =
; OTHER INFORMATION: synthetic construct

US-10-770-117-1

Query Match 100.0%; Score 47; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 1 DLMGYIPAV 9

RESULT 3
US-11-082-595-3
; Sequence 3, Application US/11082595
; Publication No. US20050163797A1
; GENERAL INFORMATION:
; APPLICANT: FLEITMANN, JULIA-KRISTINA
; APPLICANT: MATTNER, FRANK
; APPLICANT: BUSCHLE, MICHAEL
; APPLICANT: MELLING, JACK
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING AN ANTIGEN
; FILE REFERENCE: SONN:016US
; CURRENT APPLICATION NUMBER: US/11/082,595
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US/10/114,823
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: PCT/EP00/09657
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: A-1680/99
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-082-595-3

Query Match 100.0%; Score 47; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 1 DLMGYIPAV 9

RESULT 4
US-10-770-117-2
; Sequence 2, Application US/10770117
; Publication No. US20050129705A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States, as represented by the
; APPLICANT: Secretary, Dept. of
; APPLICANT: Health and Human Services
; APPLICANT: Berzofsky, Jay A.
; APPLICANT: Sarobe, Pablo
; APPLICANT: Pendleton, C. David
; APPLICANT: Feinstein, Stephen M.
; APPLICANT: Arichi, Tatsumi
; APPLICANT: Major, Marian E.
; TITLE OF INVENTION: MODIFIED HCV PEPTIDE VACCINES
; FILE REFERENCE: 14014.0347/P
; CURRENT APPLICATION NUMBER: US/10/770,117
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: US/09/763,260
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/097,446
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 8

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: synthetic construct
US-10-770-117-2

Query Match      100.0%; Score 47; DB 5; Length 191;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DLMGYIPAV 9
DB      132 DLMGYIPAV 140
|||||

RESULT 5
US-10-450-649-8
; Sequence 8, Application US/10450649
; Publication No. US20040052818A1
; GENERAL INFORMATION:
; APPLICANT: Heinz, Franz X.
; APPLICANT: Mandl, Christian
; TITLE OF INVENTION: ATTENUATED LIVE VACCINE
; FILE REFERENCE: U 014666-0
; CURRENT APPLICATION NUMBER: US/10/450,649
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/AT02/00046
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: A 272/2001 AT
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Hepatitis C Virus 2
US-10-450-649-8

Query Match      91.5%; Score 43; DB 4; Length 190;
Best Local Similarity 88.9%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 DLMGYIPAV 9
DB      131 DLMGYIPAV 139
|||||

RESULT 6
US-10-651-165-203
; Sequence 203, Application US/10651165
; Publication No. US20040047877A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 203

Query Match      91.5%; Score 43; DB 4; Length 209;
Best Local Similarity 88.9%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 DLMGYIPAV 9
DB      131 DLMGYIPAV 139
|||||

US-10-128-590-89
; Sequence 89, Application US/10128590
; Publication No. US20030108561A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Core-glycosylated HCV envelope proteins
; FILE REFERENCE: 135 PCT
; CURRENT APPLICATION NUMBER: US/10/128,590
; CURRENT FILING DATE: 2002-07-22
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 209
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-128-590-89

Query Match      91.5%; Score 43; DB 4; Length 209;
Best Local Similarity 88.9%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 DLMGYIPAV 9
DB      131 DLMGYIPAV 139
|||||
```

```
Db      ||||| |
        15 DLMGYIPV 23

RESULT 8
US-10-128-590-90
; Sequence 90, Application US/10128590
; Publication No. US20030108561A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Core-glycosylated HCV envelope proteins
; FILE REFERENCE: 135 PCT
; CURRENT APPLICATION NUMBER: US/10/128,590
; CURRENT FILING DATE: 2002-07-22
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 209
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-128-590-90

Query Match      91.5%; Score 43; DB 4; Length 209;
Best Local Similarity 88.9%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY      1 DLMGYIPAV 9
        ||||| |
Db      15 DLMGYIPV 23

RESULT 9
US-10-128-590-94
; Sequence 94, Application US/10128590
; Publication No. US20030108561A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Core-glycosylated HCV envelope proteins
; FILE REFERENCE: 135 PCT
; CURRENT APPLICATION NUMBER: US/10/128,590
; CURRENT FILING DATE: 2002-07-22
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 209
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-128-590-94

Query Match      91.5%; Score 43; DB 4; Length 209;
Best Local Similarity 88.9%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY      1 DLMGYIPAV 9
        ||||| |
Db      15 DLMGYIPV 23

RESULT 10
US-10-128-590-95
; Sequence 95, Application US/10128590
; Publication No. US20030108561A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Core-glycosylated HCV envelope proteins
; FILE REFERENCE: 135 PCT
; CURRENT APPLICATION NUMBER: US/10/128,590
; CURRENT FILING DATE: 2002-07-22
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 209
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-128-590-95

Query Match      91.5%; Score 43; DB 4; Length 209;
Best Local Similarity 88.9%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY      1 DLMGYIPAV 9
        ||||| |
Db      15 DLMGYIPV 23

RESULT 11
US-10-128-587A-89
; Sequence 89, Application US/10128587A
; Publication No. US20030152940A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Constructs and methods for expression of recombinant HCV envelope
; FILE REFERENCE: 134 PCT
; CURRENT APPLICATION NUMBER: US/10/128,587A
; CURRENT FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hepatitis C virus
US-10-128-587A-89

Query Match      91.5%; Score 43; DB 4; Length 209;
Best Local Similarity 88.9%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY      1 DLMGYIPAV 9
        ||||| |
Db      15 DLMGYIPV 23

RESULT 12
US-10-128-587A-90
; Sequence 90, Application US/10128587A
; Publication No. US20030152940A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Constructs and methods for expression of recombinant HCV envelope
; FILE REFERENCE: 134 PCT
; CURRENT APPLICATION NUMBER: US/10/128,587A
; CURRENT FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hepatitis C virus
US-10-128-587A-90

Query Match      91.5%; Score 43; DB 4; Length 209;
Best Local Similarity 88.9%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY      1 DLMGYIPAV 9
        ||||| |
Db      15 DLMGYIPV 23

RESULT 13
US-10-128-587A-90
; Sequence 90, Application US/10128587A
; Publication No. US20030152940A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Constructs and methods for expression of recombinant HCV envelope
; FILE REFERENCE: 134 PCT
; CURRENT APPLICATION NUMBER: US/10/128,587A
; CURRENT FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hepatitis C virus
US-10-128-587A-90

Query Match      91.5%; Score 43; DB 4; Length 209;
Best Local Similarity 88.9%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY      1 DLMGYIPAV 9
        ||||| |
Db      15 DLMGYIPV 23

RESULT 13
```

US-10-128-587A-94
; Sequence 94, Application US/10128587A
; Publication No. US20030152940A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Constructs and methods for expression of recombinant HCV envelope
; FILE REFERENCE: 134 PCT
; CURRENT APPLICATION NUMBER: US/10/128,587A
; CURRENT FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hepatitis C virus
US-10-128-587A-94

Query Match 91.5%; Score 43; DB 4; Length 209;
Best Local Similarity 88.9%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 15 DLMGYIPVV 23

*RESULT 14
US-10-128-587A-95
; Sequence 95, Application US/10128587A
; Publication No. US20030152940A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Constructs and methods for expression of recombinant HCV envelope
; FILE REFERENCE: 134 PCT
; CURRENT APPLICATION NUMBER: US/10/128,587A
; CURRENT FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hepatitis C virus
US-10-128-587A-95

Query Match 91.5%; Score 43; DB 4; Length 209;
Best Local Similarity 88.9%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 15 DLMGYIPVV 23

RESULT 15
US-10-651-165-204
; Sequence 204, Application US/10651165
; Publication No. US20040047877A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974,690C

; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 204
; LENGTH: 304
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-204

Query Match 91.5%; Score 43; DB 4; Length 304;
Best Local Similarity 88.9%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 132 DLMGYIPVV 140

RESULT 16
US-09-851-138-76
; Sequence 76, Application US/09851138
; Publication No. US20020183508A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,138
; FILING DATE: 09-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,075
; FILING DATE: <unknown>
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 76:
US-09-851-138-76

Query Match 91.5%; Score 43; DB 3; Length 318;
Best Local Similarity 88.9%; Pred. No. 5.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9

Db 132 DLMGYIPV 140
|||||||
RESULT 17
US-09-851-138-18
; Sequence 18, Application US/09851138
; Publication No. US20020183508A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
; AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; FILING DATE: 09-May-2001
; PRIOR APPLICATION NUMBER: US/09/851,138
; APPLICATION NUMBER: 08/836,075
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-851-138-18
Query Match 91.5%; Score 43; DB 3; Length 319;
Best Local Similarity 88.9%; Pred. No. 5.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DLMGYIPV 9
|||||||
Db 132 DLMGYIPV 140
RESULT 18
US-09-851-138-44
; Sequence 44, Application US/09851138
; Publication No. US20020183508A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
; AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433

; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; FILING DATE: 09-May-2001
; APPLICATION NUMBER: US/09/851,138
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,075
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-851-138-44
Query Match 91.5%; Score 43; DB 3; Length 319;
Best Local Similarity 88.9%; Pred. No. 5.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DLMGYIPV 9
|||||||
Db 132 DLMGYIPV 140
RESULT 19
US-09-899-046-144
; Sequence 144, Application US/09899046
; Publication No. US20030008274A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: New sequences of hepatitis C virus
; genotypes for diagnosis, prophylaxis and therapy.
; NUMBER OF SEQUENCES: 270
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,046
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/362,455
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 144:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; MOLECULE TYPE: protein
US-09-899-046-144
Query Match 91.5%; Score 43; DB 3; Length 319;
Best Local Similarity 88.9%; Pred. No. 5.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
;
;
; INFORMATION FOR SEQ ID NO: 144:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 144:
US-09-873-224-144

Query Match          91.5%; Score 43; DB 3; Length 319;
Best Local Similarity 88.9%; Pred. No. 5.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 20
US-09-878-281-144
; Sequence 144, Application US/09878281
; Publication No. US20030032005A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: New sequences of hepatitis C virus
; TYPE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy.
; NUMBER OF SEQUENCES: 270
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE:
; PRIOR APPLICATION NUMBER: US/09/878,281
; APPLICATION DATA:
; FILING DATE:
; PRIOR APPLICATION NUMBER: 08/362,455
; INFORMATION FOR SEQ ID NO: 144:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-878-281-144

Query Match          91.5%; Score 43; DB 3; Length 319;
Best Local Similarity 88.9%; Pred. No. 5.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 21
US-09-873-224-144
; Sequence 144, Application US/09873224
; Publication No. US20030064360A1
; GENERAL INFORMATION:
; APPLICANT: <Unknown>
; TITLE OF INVENTION: New sequences of hepatitis C virus
; NUMBER OF SEQUENCES: 270
; CORRESPONDENCE ADDRESS:
; STREET: Industriepark Zwijnaarde 7, box 4
; CITY: Ghent
; COUNTRY: Belgium
; ZIP: B-9052
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 05-Jun-2001
; APPLICATION NUMBER: US/09/873,224
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/362,455
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Innogenetics sa.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 00 32 9 241 07 11
; TELEFAX: 00 32 9 241 07 99
```

```
;
;
; INFORMATION FOR SEQ ID NO: 144:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 144:
US-09-873-224-144

Query Match          91.5%; Score 43; DB 3; Length 319;
Best Local Similarity 88.9%; Pred. No. 5.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 22
US-10-651-165-202
; Sequence 202, Application US/10651165
; Publication No. US20040047877A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 319
; TYPE: PRT
; ORGANISM: hepatitis C virus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (319)..(319)
; OTHER INFORMATION: Xaa is any amino acid
US-10-651-165-202

Query Match          91.5%; Score 43; DB 4; Length 319;
Best Local Similarity 88.9%; Pred. No. 5.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLMGYIPAV 9
Db 132 DLMGYIPV 140

RESULT 23
US-10-651-165-206
; Sequence 206, Application US/10651165
; Publication No. US20040047877A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
```

```
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 206
; LENGTH: 319
; TYPE: PRT
; ORGANISM: hepatitis C virus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (131)..(131)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (319)..(319)
; OTHER INFORMATION: Xaa is any amino acid
US-10-651-165-206
```

```
Query Match          91.5%; Score 43; DB 4; Length 319;
Best Local Similarity 88.9%; Pred. No. 5.7;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 DLMGYIPAV 9
Db      132 DLMGYIPV 140
```

```
RESULT 24
US-10-651-165-217
; Sequence 217, Application US/10651165
; Publication No. US2004004787A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 217
; LENGTH: 319
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-217
```

```
Query Match          91.5%; Score 43; DB 4; Length 319;
Best Local Similarity 88.9%; Pred. No. 5.7;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 DLMGYIPAV 9
Db      132 DLMGYIPV 140
```

```
RESULT 25
US-10-651-165-228
; Sequence 228, Application US/10651165
; Publication No. US2004004787A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
```

```
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 228
; LENGTH: 319
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-228
```

```
Query Match          91.5%; Score 43; DB 4; Length 319;
Best Local Similarity 88.9%; Pred. No. 5.7;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 DLMGYIPAV 9
Db      132 DLMGYIPV 140
```

```
RESULT 26
US-10-651-165-230
; Sequence 230, Application US/10651165
; Publication No. US2004004787A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 230
; LENGTH: 319
; TYPE: PRT
; ORGANISM: hepatitis C virus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (144)..(144)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (149)..(149)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (156)..(157)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (161)..(161)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (167)..(167)
; OTHER INFORMATION: Xaa is any amino acid
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; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (171)..(172)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (174)..(174)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (177)..(177)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (232)..(232)
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (233)..(233)
; OTHER INFORMATION: Xaa is any amino acid
US-10-651-165-230
```

```
Query Match          91.5%; Score 43; DB 4; Length 319;
Best Local Similarity 88.9%; Pred. No. 5.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 DLMGYIPAV 9
   |||||
Db 132 DLMGYIPV 140
```

```
RESULT 27
US-10-651-165-200
; Sequence 200, Application US/10651165
; Publication No. US2004004787A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 200
; LENGTH: 450
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-200
```

```
Query Match          91.5%; Score 43; DB 4; Length 450;
Best Local Similarity 88.9%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 DLMGYIPAV 9
   |||||
Db 132 DLMGYIPV 140
```

```
RESULT 28
US-10-651-165-201
; Sequence 201, Application US/10651165
; Publication No. US2004004787A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
```

```
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 201
; LENGTH: 450
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-201
```

```
Query Match          91.5%; Score 43; DB 4; Length 450;
Best Local Similarity 88.9%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 DLMGYIPAV 9
   |||||
Db 132 DLMGYIPV 140
```

```
RESULT 29
US-10-226-629A-13
; Sequence 13, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 2940
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-226-629A-13
```

```
Query Match          91.5%; Score 43; DB 4; Length 2940;
Best Local Similarity 88.9%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 DLMGYIPAV 9
   |||||
Db 132 DLMGYIPV 140
```

```
RESULT 30
US-08-854-825-54
; Sequence 54, Application US/08854825
; Publication No. US20020115061A1
; GENERAL INFORMATION:
; APPLICANT: Chisari, Francis V.
; APPLICANT: Cerny, Andreas
; TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T
; TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
```

```

; ADDRESSES: Leydig, Voit & Mayer
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,825
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silvert, Donald J.
; REGISTRATION NUMBER: 37552
; REFERENCE/DOCKET NUMBER: 61230
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-854-825-54

Query Match 89.4%; Score 42; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
DB 1 DLMGYIPLV 9

RESULT 31
US-09-894-018-212
; Sequence 212, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Deniaw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 212
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Transgenic mouse
; US-09-894-018-212

Query Match 89.4%; Score 42; DB 3; Length 9;

; ADDRESSES: Leydig, Voit & Mayer
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,825
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silvert, Donald J.
; REGISTRATION NUMBER: 37552
; REFERENCE/DOCKET NUMBER: 61230
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-854-825-54

Query Match 89.4%; Score 42; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
DB 1 DLMGYIPLV 9

RESULT 32
US-10-128-711-51
; Sequence 51, Application US/10128711
; Publication No. US20030099634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-10-128-711-51

Query Match 89.4%; Score 42; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
DB 1 DLMGYIPLV 9
```

RESULT 33
US-10-128-711-130
; Sequence 130, Application US/10128711
; Publication No. US20030099634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend Khourie and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 130:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 130:
US-10-128-711-130

Query Match 89.4%; Score 42; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
| | | | | | | |
Db 1 DLMGYIPLV 9

RESULT 34
US-10-114-823B-20
; Sequence 20, Application US/10114823B
; Publication No. US20030099663A1
; GENERAL INFORMATION:
; APPLICANT: FLEITMANN, JULIA-KRISTINA

; APPLICANT: MATTNER, FRANK
; APPLICANT: BUSCHLE, MICHAEL
; APPLICANT: MELLING, JACK
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING AN ANTIGEN
; FILE REFERENCE: SONN:016US
; CURRENT APPLICATION NUMBER: US/10/114,823B
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: PCT/EP00/09657
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: A-1680/99
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-114-823B-20

Query Match 89.4%; Score 42; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
| | | | | | | |
Db 1 DLMGYIPLV 9

RESULT 35
US-10-371-525-255
; Sequence 255, Application US/10371525
; Publication No. US20030203869A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Cheenut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/10/371,525
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/311,784
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 255
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV Core 132 (peptide 1013.1002)
US-10-371-525-255

Query Match 89.4%; Score 42; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
| | | | | | | |
Db 1 DLMGYIPLV 9

RESULT 36
US-10-371-069-255

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; Sequence 255, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 255
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV Core 132 (peptide 1013.1002)
; US-10-371-069-255

Query Match      89.4%; Score 42; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      1 DLMGYIPAV 9
      |||||
Db      1 DLMGYIPLV 9

RESULT 37
US-10-371-645-255
; Sequence 255, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 255
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV Core 132 (peptide 1013.1002)
; US-10-371-645-255

Query Match      89.4%; Score 42; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      1 DLMGYIPAV 9
      |||||
Db      1 DLMGYIPLV 9

*RESULT 37
US-10-371-645-255
; Sequence 255, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 255
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV Core 132 (peptide 1013.1002)
; US-10-371-645-255

Query Match      89.4%; Score 42; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      1 DLMGYIPAV 9
      |||||
Db      1 DLMGYIPLV 9

US-10-371-260-255
; Sequence 255, Application US/10371260
; Publication No. US20030220285A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.13
; CURRENT APPLICATION NUMBER: US/10/371,260
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 255
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV Core 132 (peptide 1013.1002)
; US-10-371-260-255

Query Match      89.4%; Score 42; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      1 DLMGYIPAV 9
      |||||
Db      1 DLMGYIPLV 9

RESULT 39
US-10-367-580-74
; Sequence 74, Application US/10367580
; Publication No. US20040071720A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461061
; CURRENT APPLICATION NUMBER: US/10/367,580
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,832
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
```

;/ NUMBER OF SEQ ID NOS: 349
;/ SOFTWARE: WordPerfect 8.0 for Windows
;/ SEQ ID NO 74
;/ LENGTH: 9
;/ TYPE: PRT
;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: synthetic peptide
US-10-367-580-74

Query Match 89.4%; Score 42; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
| | | | |
Db 1 DLMGYIPLV 9

RESULT 40
US-10-367-593-74
;/ Sequence 74, Application US/10367593
;/ Publication No. US20040071721A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Rothman, James E.
;/ APPLICANT: Hartl, F. Ulrich
;/ APPLICANT: Hoe, Mee H.
;/ APPLICANT: Houghton, Alan
;/ APPLICANT: Takechi, Yoshizumi
;/ APPLICANT: Mayhew, Mark
;/ TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
;/ FILE REFERENCE: 11746/461012
;/ CURRENT APPLICATION NUMBER: US/10/367,593
;/ CURRENT FILING DATE: 2003-02-14
;/ PRIOR APPLICATION NUMBER: US 09/011,645
;/ PRIOR FILING DATE: 1998-02-13
;/ PRIOR APPLICATION NUMBER: PCT/US96/13363
;/ PRIOR FILING DATE: 1996-08-16
;/ PRIOR APPLICATION NUMBER: US 60/002,490
;/ PRIOR FILING DATE: 1995-08-18
;/ PRIOR APPLICATION NUMBER: US 60/002,479
;/ PRIOR FILING DATE: 1995-08-18
;/ NUMBER OF SEQ ID NOS: 349
;/ SOFTWARE: WordPerfect 8.0 for Windows
;/ SEQ ID NO 74
;/ LENGTH: 9
;/ TYPE: PRT
;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: synthetic peptide
US-10-367-593-74

Query Match 89.4%; Score 42; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLMGYIPAV 9
| | | | |
Db 1 DLMGYIPLV 9

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Job time : 118 secs

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